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nucleic - nucleic search, using sw model
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September 24, 2004, 01:07:51, Search time 228 Seconds
(11/11/2004)
8291.912 Million call updates/sec

File: US-08-964-277-20
Left score: 35.37
Sequence: 1 GGGAGGAGGAGGAGATA.....ATGAAGTGAAGCTGGTC 3332
Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0
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[illegible]

[illegible]

Qy 1124 CACTGTTCAGTGGATCTCCGCTCCGCAACATCGTCTACCTGCTCATCATGAGAGG 1183
 Db 978 CACTGCTTCGCGGGGGTGGCGCTTCCTGCAACCTGCTGCTGCTTCTGCTGAGAG 1037
 Qy 1184 ATGACAGATGCTTTAGATGAGTTCAGAGATTTGGAAGAAAAGAGCTACTATATCT 1243
 Db 1038 CTCACCTCTCTCTACACAGTCTCTAGCTCTGCTGCTGAGAGAGAGTCTTACCTCTCC 1097
 Qy 1244 CCACATCTTCTTCGCGCAACCTGCTGAGCTATGAG 1282
 Db 1098 CCCAACTTCACATCTTCATGCGGGCAGTCTGCACTTTGAG 1136

RESULT 7
 US-09-023-655-347
 / Sequence 347, Application US/09023655
 / Patent No. 6509338
 / GENERAL INFORMATION:
 / APPLICANT: Cocks, Benjamin G.
 / APPLICANT: Susan G. Stuart
 / APPLICANT: Jeffrey J. Sellman
 / TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
 / NUMBER OF SEQUENCES: 1508
 / CORRESPONDENCE ADDRESS:
 / ADDRESS: INCITE PHARMACEUTICALS, INC.
 / STREET: 3174 PORTER DRIVE
 / CITY: PALO ALTO
 / STATE: CALIFORNIA
 / COUNTRY: USA
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: Microsoft Perfect 6.1 for Windows/MS-DOS 6.2
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/09/023,655
 / FILING DATE: HEREWITH
 / CLASSIFICATION: DATA:
 / PRIORITY APPLICATION NUMBER:
 / FILING DATE:
 / CLASSIFICATION:
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Zeller, Karen J.
 / REGISTRATION NUMBER: 37,071
 / REFERENCE/DOCKET NUMBER: PA-0001 US
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: (650) 845-4165
 / TELEFAX: (650) 845-4166
 / INFORMATION FOR SEQ ID NO: 347:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 1208 base pairs
 / STRANDEDNESS: single
 / TOPOLOGY: linear
 / IMMEDIATE SOURCE:
 / LIBRARY: THERMOT03
 / CLONE: 9414845
 / US-09-023-655-347

Query Match 2.89; Score 94.6; DB 4; Length 1208;
 Identical Similarity 64.34; Pct. No. 6.66-19;
 Mismatches 147; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
 Qy 1077 TAGATTCATATGAGAGAGCAAGCTCCCAATGATGTGTTAGTCACTTTAGTCG 1136
 Db 4 TTGAGTTTATTAGAGAGCTCCCAATGATGTGTTAGTCACTTTAGTCACTTCGCTG 63
 Qy 1137 GCATCTCCGCTCCGCAACCTGCTATCCATCATGAGAGATGACATGCTT 1196

Db 64 GCGTGTCCGCTCCGCAACATCGTCTACCTGATGAAGCACTCGATGACCA 123
 Qy 1197 TAGATGAGCTTCAGTTCATGATGAGAGAGAGAGAGCTACTATATTCGCAACTCAAT 1256
 Db 124 TGATGATCTTCTTAATTTCTTCAAGGCAAGCAACCTACTTCTCCCAACCTTACT 183
 Qy 1257 TTTCTGGCCCAACTCTGCTGATCATGATGAGAGAGATTAAGAC 1297
 Db 184 TCTGCGGCGCTCTGCTGATGCTCGAGAGAGCTTAAACAC 224

RESULT 8
 US-09-016-434-1135
 / Sequence 1135, Application US/09016434
 / Patent No. 6509338
 / GENERAL INFORMATION:
 / APPLICANT: Janice Au-Yang
 / APPLICANT: Jeffrey J. Sellman
 / TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
 / NUMBER OF SEQUENCES: 1490
 / CORRESPONDENCE ADDRESS:
 / ADDRESS: INCITE PHARMACEUTICALS, INC.
 / STREET: 3174 PORTER DRIVE
 / CITY: PALO ALTO
 / STATE: CALIFORNIA
 / COUNTRY: USA
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: Microsoft Perfect 6.1 for Windows/MS-DOS 6.2
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/09/016,434
 / FILING DATE: HEREWITH
 / CLASSIFICATION: DATA:
 / PRIORITY APPLICATION NUMBER:
 / FILING DATE:
 / CLASSIFICATION:
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Zeller, Karen J.
 / REGISTRATION NUMBER: 37,071
 / REFERENCE/DOCKET NUMBER: PA-0002 US
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: (650) 845-4165
 / TELEFAX: (650) 845-4166
 / INFORMATION FOR SEQ ID NO: 1135:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 1208 base pairs
 / STRANDEDNESS: single
 / TOPOLOGY: linear
 / IMMEDIATE SOURCE:
 / LIBRARY: THERMOT03
 / CLONE: 9414893
 / US-09-016-434-1135

Query Match 2.78; Score 89.2; DB 4; Length 2109;
 Identical Similarity 57.18; Pct. No. 2.56-17;
 Mismatches 164; Conservative 0; Mismatches 123; Indels 0; Gaps 0;
 Qy 1004 GAGTCTATTCCTGCTGCTGCTGATGACAGCTTTTGTGAGAAATTTCCCTGCG 1063
 Db 1105 GAGTTATTAATGACAAATCCCATCTCGATCTTGGAGCCAACTCTCCCAATTT 1164
 Qy 1064 TTGGCAAAATCAGTATGATTCATTTGAGAGAGAGAGCTCCCAATGATGTCTTAGT 1123
 Db 1165 TTCTTGAGCTCTTCTTTTATGATGAGAGCCGAGAGAGCTGTGCTTTGATA 1224
 Qy 1124 CATGTTTAGTGGATCTTCCTGCTCCGACATCTGCTTACTATCATATGAGAGG 1183

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APPLICANT: Fanger, Gary
APPLICANT: Fanger, Gary
APPLICANT: Gertter, Marc
APPLICANT: Gertter, Marc
APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TREATMENT OF LUNG CANCER
FILE REFERENCE: 210121.478C12
CURRENT APPLICATION NUMBER: US/09/671.325
PUBLICATION NUMBER: 2009/020397-A1
NUMBER OF SEQ ID NOS: 1025
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 801
SEQUENCE INFORMATION
TYPE: DNA
ORGANISM: Homo sapien
8-09-671-325-801
Query Match
Best Local Similarity 5.6%; Score 85.6; DB 4; Length 1619;
Matches 178; Conservative 0; Mismatches 154; Indels 0; Gaps 0
y 993 ACTTTTACCCGAGCGATCATCTGCTGGGCGGCGCTGATGCTGTGGAGAAA 1052
425 ACTTTTGAAGAGCATATCATCAGTGCATCCAGTGGAGATATCACAGACGCA 1488
y 1053 TTTTCGCTGGTGGACAAAGTCAAGTATNTTGTGGAGAAAGAAAGCTCTCAAGT 1112
y 489 TGAAGTCTCTTGTATCATGAGAGCATAGAGTACATGATGATGAGAGCTGCTGGG 548
y 1113 GGTGTCATATGATGATCTTTAGTATGAGAGATTCCTGCTGCTGCTGCTGCTG 1172
549 GGTGTCATATGATGATCTTTAGTATGAGAGATTCCTGCTGCTGCTGCTGCTG 1172
608 TTTTCGCTGGTGGACAAAGTCAAGTATNTTGTGGAGAAAGAAAGCTCTCAAGT

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USULT 3
 Sequence 26334, Application US/10425114
 Application Number: 104093486A
 GENERAL INFORMATION
 APPLICANT: Liu, Jingtong
 APPLICANT: Zhou, Yihua
 APPLICANT: Zhang, David X.
 APPLICANT: Screen, Steven E
 APPLICANT: Tabaska, Jack E
 APPLICANT: Cao, Yonpei
 TITLE OF INVENTION: Purine and Pyrimidine Acid Molecules Associated With
 Purine and Pyrimidine Nucleosides and Uses Thereof for Plant Improvement

APPLICANT: CBO, Yoshimi
 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 The Regulation of Plant Growth and Uses Thereof for Plant Improvement
 FILE REFERENCE: 39-215313.13
 CURRENT APPLICATION NUMBER: US/10/425,114
 CURRENT FILING DATE: 2003-04-28
 NUMBER OF SEQ ID NOS: 73128
 SEQ ID NO 26234
 LENGTH: 3625

TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Clone ID: LIB4119-028-H6_FLI
5'-10-425-114-56234

Query Match	94.4%	Score 3145;	DB 13;	Length 3625;
Best Local Similarity	95.3%	Pred. No. 0;		
Matches 3330: Conservative	0:	Mismatches	0:	Indels 165; Gaps 2;

2 AGAGAAGGAGMGATTAATATATCTGAAAAGAAGAGGAGGAGGAGAGCGGACGCGGACG 61
132 AGAGAAGGAGAGAGATTAATATCTGAAAAGAAGAGGAGGAGGAGAGCGGACGCGGACG 191

62 CGAGCGGAGCGCAGCGCCCTCTGGCTCGGGCGGCGCTCGCAAGTCGGGAGGG 121
|||
192 CGAGTCGAGCGCAGCGCCCTCTGGTTCGGCGGGCGGCTCGCAAGTCGGGAGGG 251
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122 AGGGGGCCGAGGGGAGAGCCCGTGAACAATTTCGTTTCCTCTGAGGGAATTGGGAGG 181

252 AGGGGGCCCGAGGGGAGAGCCCGTGAACAATTTCGTTTCCTCTGAGGGAATTGGGAGG 311

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Db	1392	AAGCTTCGAACTGATGTTCTAGTGCACTGTTTAGCTGGGATCTCCGCTCCGCAACA	1451		2238	ATGAGAGAGCCCTCTTGAAAGACCACTTAAAGCAGAGAGTGCCTCAATGSAATTTGGAG	2297		
Qy	1158	TGCTGATCGCTCATCATGATGAGAGATGAGATGATCTTTAGATGAAGCTTACAGATTG	1217		Db	2532	ATGAGAGAGCCCTCTTGAAAGACCACTTAAAGCAGAGAGTGCCTCAATGSAATTTGGAG	2591	
Db	1452	TGCTGATCGCTCATCATGATGAGAGATGAGATGATCTTTAGATGAAGCTTACAGATTG	1511		Qy	2298	AGAGCATCATCTGAGAGAACAGATGATCGGAGAGAGTGGGAGATGCGGCACTGATTA	2357	
Qy	1218	TGAGAGAGAGAGAGCTACTATATCTCCAAATCTTAATTTCTGGGCAATCTGSACT	1277		Db	2592	AGAGCATCATCTGAGAGAACAGATGATCGGAGAGAGTGGGAGATGCGGCACTGATTA	2651	
Db	1512	TGAGAGAGAGAGAGCTACTATATCTCCAAATCTTAATTTCTGGGCAATCTGSACT	1571		Qy	2358	CGTTTGGGAGAGAGAGTGGGAGATGATGAGAGTCTCTGAGAGAGAGAGAGAGAGAGAG	2417	
Qy	1278	ATGAGAGAGAGAGAGCTACTATATCTCCAAATCTTAATTTCTGGGCAATCTGSACT	1337		Db	2652	CGTTTGGGAGAGAGAGTGGGAGATGATGAGAGTCTCTGAGAGAGAGAGAGAGAGAGAG	2711	
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Qy	1338	TGCTGATCGCTCATCATGATGAGAGATGAGATGATCTTTAGATGAAGCTTACAGATTG	1397		Db	2712	TATGAG	2771	
Db	1632	TGCTGATCGCTCATCATGATGAGAGATGAGATGATCTTTAGATGAAGCTTACAGATTG	1691		Qy	2478	TGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	2537	
Qy	1398	AGAGCTTCGAACTGATGTTCTAGTGCACTGTTTAGCTGGGATCTCCGCTCCGCAACA	1457		Db	2772	TGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	2831	
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Qy	1518	CGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1577		Db	2832	ACCGAGTGTGATCT	2891	
Db	1812	CGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1871		Qy	2598	AAATGAG	2657	
Qy	1578	ATGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1637		Db	2892	AAATGAG	2951	
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Db	2111	CGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	2171		Qy	2898	AAACCAAG	2957	
Qy	2171	CGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	2231		Db	3191	AAACCAAG	3250	
Db	2231	CGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	2291		Qy	2958	GGGGCTCTGCGCAAGGCTTACTTATGAGAGAACCAAGCTTACTCTCAGAGACAGAAAGTGGGGC	3017	
Qy	2291	CGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	2351		Db	3251	GGGGCTCTGCGCAAGGCTTACTTATGAGAGAACCAAGCTTACTCTCAGAGACAGAAAGTGGGGC	3310	
Db	2351	CGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	2411		Qy	3018	TTTTGGCTCTGCGCAAGGCTTACTTATGAGAGAACCAAGCTTACTCTCAGAGACAGAAAGTGGGGC	3077	
Qy	2411	CGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	2471		Db	3311	TTTTGGCTCTGCGCAAGGCTTACTTATGAGAGAACCAAGCTTACTCTCAGAGACAGAAAGTGGGGC	3370	
Db	2471	CGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	2531		Qy	3078	GTGAGCTTCTGAG	3137	
Qy	2531	CGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	2591		Db	3137	GTGAGCTTCTGAG	3196	
Db	2591	CGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	2651		Qy	3198	GTGAGCTTCTGAG	3257	
Qy	2651	CGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	2711		Db	3491	GTGAGCTTCTGAG	3550	
Db	2711	CGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	2771		Qy	3258	ACCT	3317	

Db 1321 AGGATGAGACGTCCTTAGATGAGCTTACAGATTGTGGAAGAAAAGACCTACTATA 1330
 Qy TCTCCAAATCTAAATTTTCTGGCCGAACTCTCTGAGCTATGAGAGAGATTAGGAACG 1340
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 Qy 1541 AGCTGTGCGCAGCTGTGAG 1600
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 Db 2281 TACAG 2340
 Qy 2201 AAGCAG 2260
 Db 2341 AAGCAG 2400
 Qy 2261 CAGTGTGAG 2320
 Db 2401 CAGTGTGAG 2460

ORGANISM: Homo Sapiens

FEATURE: Cons

NAME/ID: US9... (2586)

1-10-377-072-25

Query Match: 88.5%; Score 2950; DB 16; Length 3544;

Seq. Ids: 100%; Pos: 100%;

Matches 3135; Conservative: 0; Mismatches 165; Gaps 2;

1 197 GTTTCATGCGTGTGAAAGCTGTGGAGCGGGAGCAAGGTAAAGATGATGATG 256
 2 198 GTTTCATGCGTGTGAAAGCTGTGGAGCGGGAGCAAGGTAAAGATGATGATG 257
 3 224 GTTTCATGCGTGTGAAAGCTGTGGAGCGGGAGCAAGGTAAAGATGATGATG 283
 4 257 CGCTGGCTGCTCAAGACATCTTTGTGTGATGTATTCAGTATCTCTTATGA 316
 5 284 GTTTCATGCGTGTGAAAGCTGTGGAGCGGGAGCAAGGTAAAGATGATGATG 343
 6 317 ATCAAAATCTGAGGGGCTGTTGTGTGAGAGTCTTTGTGAAAGACATCAAGGAAA 376
 7 344 ATCAAAATCTGAGGGGCTGTTGTGTGAGAGTCTTTGTGAAAGACATCAAGGAAA 403
 8 377 GAGAGAGAGCAATTCATCTGGAGGGCTCTGCTGAATATGGTATTACTCTCTTGGC 436
 9 404 GAGAGAGAGCAATTCATCTGGAGGGCTCTGCTGAATATGGTATTACTCTCTTGGC 463
 10 437 AGTACACAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 496
 11 464 AGTACACAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 523
 12 497 AGCAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 556
 13 524 AGCAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 583
 14 557 TTGTATGAGCCATGAGATGATGATGATGATGATGATGATGATGATGATGATG 616
 15 584 TTGTATGAGCCATGAGATGATGATGATGATGATGATGATGATGATGATGATG 643
 16 617 TGGAAAGTGGAGCGGAAAGAGCTGCTGATGATGAGCGGCAATTTGTGAAATCAATA 676
 17 644 TGGAAAGTGGAGCGGAAAGAGCTGCTGATGATGAGCGGCAATTTGTGAAATCAATA 703
 18 677 CATCCACATTTTGGAGCGCATTAATTAACCTGCTCCAGCTATGAGAGAGGTTCG 736
 19 704 CATCCACATTTTGGAGCGCATTAATTAACCTGCTCCAGCTATGAGAGAGGTTCG 763
 20 737 ACAGGACAGATGTTTAATTCAGAGCTCATCAGCATCATCAGCATCATCAGGTTCG 796
 21 764 ACAGGACAGATGTTTAATTCAGAGCTCATCAGCATCATCAGCATCATCAGGTTCG 823
 22 797 TTGTATGAGCCATGAGATGATGATGATGATGATGATGATGATGATGATGATG 856
 23 824 TTGTATGAGCCATGAGATGATGATGATGATGATGATGATGATGATGATGATG 883
 24 857 GTTTCATGCGTGTGAAAGCTGTGGAGCGGGAGCAAGGTAAAGATGATGATG 916
 25 884 GTTTCATGCGTGTGAAAGCTGTGGAGCGGGAGCAAGGTAAAGATGATGATG 943
 26 917 ACCTGCTTCG----- 926
 27 944 ACCTGCTTCG----- 926
 28 927----- 927
 29 1004 ATTCACATCTAGTCCCTACCTGCAATTTCTGAGCTTGTCTACTGTGCGAATTTGGCG 1063
 30 927----- 927
 31 1064 CAAACCGAATCTTCCCATCTTTATCTTGGCTGCGAGAGATGTTCTCAACAGAGCTG 1123
 32 933 TGTGAGCAGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 992
 33 1124 TGTGAGCAGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1183

Oy 993 ACTTATACCCGAGTCTATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1052
 Db 1184 ACTTATACCCGAGTCTATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1243
 Oy 1053 TTTTTCGCTGTGTGAGCAATCTAGTATGATTTATTTATGAAAGAAAGAGCTCTATGAT 1112
 Db 1244 TTTTTCGCTGTGTGAGCAATCTAGTATGATTTATTTATGAAAGAAAGAGCTCTATGAT 1303
 Oy 1113 GGTGCTTAGTGATCTTTAGCTTGGAGTCTCCGCTCCGCAACATCTGATCGCTACCA 1172
 Db 1304 GGTGCTTAGTGATCTTTAGCTTGGAGTCTCCGCTCCGCAACATCTGATCGCTACCA 1363
 Oy 1173 TATGATGAGAGTGAAGATGATCTTTTATGATGAGCTTACAGATTTGTGAAGAAAGAGC 1232
 Db 1423 TATGATGAGAGTGAAGATGATCTTTTATGATGAGCTTACAGATTTGTGAAGAAAGAGC 1483
 Oy 1233 CTACTATATCTCAAATCTCAATTTCTGGGCAACTCTGAGATATGAGAGAGATTA 1292
 Db 1424 CTACTATATCTCAAATCTCAATTTCTGGGCAACTCTGAGATATGAGAGAGATTA 1483
 Oy 1293 AGAACCCAGCTGAGCACTCAGGCTCAAGAGCAACTCAAGCTGTGCTGCTGAGAGG 1352
 Db 1484 AGAACCCAGCTGAGCACTCAGGCTCAAGAGCAACTCAAGCTGTGCTGCTGAGAGG 1543
 Oy 1353 CAATTAAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1412
 Db 1544 CAATTAAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1603
 Oy 1413 CAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1472
 Db 1604 CAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1663
 Oy 1473 GCTGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1532
 Db 1664 GCTGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1723
 Oy 1533 CGCTCAGTGGGCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1592
 Db 1724 CGCTCAGTGGGCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1783
 Oy 1593 CTTCTCTCTGATATCAATCAATGTTTATATTCAGCTCAGCATGAGCATCTTATGATG 1652
 Db 1784 CTTCTCTCTGATATCAATCAATGTTTATATTCAGCTCAGCATGAGCATCTTATGATG 1843
 Oy 1653 GCTTCTCTCTATGAGAGTCTTTTGGATATCTACAACTTCTCACTCTGAGTGGGA 1712
 Db 1844 GCTTCTCTCTATGAGAGTCTTTTGGATATCTACAACTTCTCACTCTGAGTGGGA 1903
 Oy 1713 GCAACAGCTATGCTCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1772
 Db 1904 GCAACAGCTATGCTCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1963
 Oy 1773 GTCTCTATGAGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 1832
 Db 2023 GTCTCTATGAGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 2083
 Oy 1833 GCGAGGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1892
 Db 2084 GCGAGGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2143
 Oy 1893 TTTTATCTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 1952
 Db 2143 TTTTATCTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 2203
 Oy 1953 TGCGCTTCTCCACGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 2012
 Db 2203 TGCGCTTCTCCACGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 2263
 Oy 2012 GGCATCTGGATATCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2072
 Db 2263 GGCATCTGGATATCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2323

[illegible]

1364	db	TCCTGAGAGAGTGGACATGCTCTTATGAGTGAAGCTTACACGATTTGTGAGAGAAAGAC	1413
1233	zy	CTACTATATCTCCAAATCTCAATATTTCTTGGGCGAACTCTCTGGATCTGTGAGAGAGATTA	1292
1424	db	CTACTATATCTCCAAATCTCAATATTTCTTGGGCGAACTCTCTGGATCTGTGAGAGAGATTA	1483
1293	zy	CTACTATATCTGGACATCAATGCGGCGAACTCAAGCTCTGCGATCTGGAGAGAGC	1352
1484	db	CTACTATATCTGGACATCAATGCGGCGAACTCAAGCTCTGCGATCTGGAGAGAGC	1543
1353	zy	CAATATGAGAGAGTGGCTCTCTCTGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGC	1412
1544	db	CAATATGAGAGAGTGGCTCTCTCTGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGC	1603
1413	zy	CAGCTCTGTCGCGATCTCTCTTACTCTCAGAGGACACCGAGCAAAAGAGCTGTGATCTGCCA	1472
1604	db	CAGCTCTGTCGCGATCTCTCTTACTCTCAGAGGAGAGAGAGAGAGAGAGAGAGAGAGC	1663
1473	zy	GCGGTGTCGAGAGCTGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC	1532
1664	db	GCGGTGTCGAGAGCTGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC	1723
1533	zy	CGCTCAAGTGGCTGACCTGTCTCCGACAGAGCTGGAGACAGAGATTAAGCTCAAGAGCTT	1592
1724	db	CGCTCAAGTGGCTGACCTGTCTCCGACAGAGCTGGAGACAGAGATTAAGCTCAAGAGCTT	1783
1593	zy	CTCTCTCTGCGATATCAAAATCTGATATTCAGCTGAGCTATGCGGAGCTATGCTCATGTC	1653
1784	db	CTCTCTCTGCGATATCAAAATCTGATATTCAGCTGAGCTATGCGGAGCTATGCTCATGTC	1843
1653	zy	GGTCTCTGCTGCGAGATTCCTTGTGGATATCTCAAAAGAGCTGCTCATCTGTGGAGAGGA	1712
1844	db	GGTCTCTGCTGCGAGATTCCTTGTGGATATCTCAAAAGAGCTGCTCATCTGTGGAGAGGA	1903
1713	zy	CCAAACAGATATGCGAGTTCTCTCCCTCTGTGAGAGCTATGTGAGAGAGCTCTCGAAACCA	1772
1904	db	CCAAACAGATATGCGAGTTCTCTCCCTCTGTGAGAGCTATGTGAGAGAGCTCTCGAAACCA	1963
1773	zy	GTCTCTGATTAAGGAGAGAGCAGCATCTCCCAAGAGAGCTGACAGCGGACGGGCTCTCAGCA	1832
1964	db	GTCTCTGATTAAGGAGAGAGCAGCATCTCCCAAGAGAGCTGACAGCGGACGGGCTCTCAGCA	2023
1833	zy	GCGAGCAGCAGCATGTGATCTGGTGTGAGACAGAGCTGAGACAGCGCCGAGAGGTCCTC	1892
2024	db	GCGAGCAGCAGCATGTGATCTGGTGTGAGACAGAGCTGAGACAGCGCCGAGAGGTCCTC	2083
1893	zy	TTTATATCTGAGCTGTGATCTGGTGTGAGACAGAGCTGAGACAGCGCCGAGAGCTCTTT	1953
2084	db	TTTATATCTGAGCTGTGATCTGGTGTGAGACAGAGCTGAGACAGCGCCGAGAGCTCTTT	2143
1953	zy	TGCGCTTTTCCACGCGAGCGAGCATCTGAGAGCTCTGTGCTGTGGCTGTGAGAGAGCTT	2012
2144	db	TGCGCTTTTCCACGCGAGCGAGCATCTGAGAGCTCTGTGCTGTGGCTGTGAGAGAGCTT	2203
2013	zy	GGCATCTGGATATCTTGGCGCCCGACACCTTCTACCTCTCTCTGACGCGAGAGCTGGATAT	2072
2204	db	GGCATCTGGATATCTTGGCGCCCGACACCTTCTACCTCTCTCTGACGCGAGAGCTGGATAT	2263
2073	zy	TGGCCACAGAGCTCTCAGAGCTCTACTCTGCTCTCAGCTCTGAGCGATCTGAGGAGAGTCGAGTT	2133
2264	db	TGGCCACAGAGCTCTCAGAGCTCTACTCTGCTCTCAGCTCTGAGCGATCTGAGGAGAGTCGAGTT	2323
2133	zy	ACTGTGCTCTACAGCTGCGAGCTGCGAGCGCCACTTGGGAGAGCAGATCTTATCTGTGGCA	2192
2324	db	ACTGTGCTCTACAGCTGCGAGCTGCGAGCGCCACTTGGGAGAGCAGATCTTATCTGTGGCA	2383
2193	zy	GGCGGCTGAGCGATGAGACAGAGCTGCGAGCTGCGAGCTGCGAGCTGCGAGAGAGCTCTT	2253
2384	db	GGCGGCTGAGCGATGAGACAGAGCTGCGAGCTGCGAGCTGCGAGCTGCGAGAGAGCTCTT	2443
2253	zy	TTGAAAGAGATTTAAAGCGAGAGAGCTGCGAAATGGATTTGGAGAGAGATCATGTGAG	2312
2444	db	TTGAAAGAGAGCTTTAAAGCGAGAGAGAGCTGCGAAATGGATTTGGAGAGAGATCATGTGAG	2503

Qy 3155 TCTGCTTTATGAGAGAGGAGAACTGTCTAGAGTTCTGAGTCTGAACCGAGACCTG 3214
 Db 2940 TCTGCTTTATGAGAGAGGAGAACTGTCTAGAGTTCTGAGTCTGAACCGAGACCTG 2999
 Qy 3215 GCAATCATCAGATTAAGCTTTGGAGGCAACGAGTCTGCTCTCTCTTTGAAA 3274
 Db 3000 GCAATCATCAGATTAAGCTTTGGAGGCAACGAGTCTGCTCTCTCTTTGAAA 3059
 Qy 3275 TCAAGAGTTTAAATGGGATTTGCAATCTTAAATAGAGTGAAGTCTTTC 3332
 Db 3060 TCAAGAGTTTAAATGGGATTTGCAATCTTAAATAGAGTGAAGTCTTTC 3117

RESULT 9

US-10-257-026-1
 ; Sequence 1: Application US/10257026
 ; Sequence 2: Application US/00408659A1
 ; GENERAL INFORMATION
 ; APPLICANT: Merck Patent GmbH
 ; TITLE OF INVENTION: New dual specificity phosphatase
 ; INVENTOR: MERCK PATENT GMBH
 ; CURRENT PILING DATE: 2003-11-07
 ; NUMBER OF SEQ ID NOS: 3
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NOS: 3059
 ; LENGTH: 3059
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURES: CDS
 ; LOCATION: (127)..(2121)
 ; US-10-257-026-1

Query Match
 Similarity 81.34; Score 2710; DB 17; Length 3059;
 Percent 84.4; 0; Mismatches 0; Indels 165; Gaps 2;
 Matches 2895; Conservative

Qy 436 CAGTCACACAGGCTGACCTGATCACTTTTATGATGAGTGTGAGGCTTGG 495
 Db 1 CAGTCACACAGGCTGACCTGATCACTTTTATGATGAGTGTGAGGCTTGG 60
 Qy 496 CACACCATCATCATCTGCGCAATTAAGAGAGAGTGGGAAGAGACTTAT 555
 Db 61 CACACCATCATCATCTGCGCAATTAAGAGAGAGTGGGAAGAGACTTAT 120
 Qy 556 GTTCTGATGCGCCATGAGATGATGGAATCAATTTGTTACTGAGAGTGGTGGTCTG 615
 Db 111 GTTCTGATGCGCCATGAGATGATGGAATCAATTTGTTACTGAGAGTGGTGGTCTG 180
 Qy 616 CTGGAAGTGGCAAGGAAGTGTCTTAATGACGCGCCATTTGTTGATGATCAT 675
 Db 181 CTGGAAGTGGCAAGGAAGTGTCTTAATGACGCGCCATTTGTTGATGATCAT 240
 Qy 676 ACATTCACATTTGGAGACCATTAATTCATCTGTCGACATTTAGAGAGAGTGTG 735
 Db 241 ACATTCACATTTGGAGACCATTAATTCATCTGTCGACATTTAGAGAGAGTGTG 300
 Qy 736 CAGAGCAAGATTTTATGAGATGATGAGATGATGAGATGATGAGATGATGAG 795
 Db 301 CAGAGCAAGATTTTATGAGATGATGAGATGATGAGATGATGAGATGATGAG 420
 Qy 796 ATGATTCGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 855
 Db 361 ATGATTCGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
 Qy 856 TCTTTCAGATGTTTCTCATCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 915
 Db 421 TCTTTCAGATGTTTCTCATCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
 Qy 916 CACCTGCTTGC ----- 926
 Db 481 CACCTGCTTGCAGTGGTGTGAGATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540

Qy 927 ----- 926
 Db 541 AATTCGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAG 600
 Qy 927 ----- AGAG 931
 Db 601 CGAACCGGATTTTCCCATCTTTTATCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
 Qy 932 CTGATGCTGAGATGAGATGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 991
 Db 661 CTGATGCTGAGATGAGATGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
 Qy 992 GACTTATATCCCGAGCTCAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1051
 Db 721 GACTTATATCCCGAGCTCAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
 Qy 1052 ATTCTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1111
 Db 781 ATTCTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
 Qy 1112 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1171
 Db 841 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
 Qy 1172 ATATGAGAGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATG 1231
 Db 901 ATATGAGAGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATG 960
 Qy 1232 CTTATATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1291
 Db 961 CTTATATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
 Qy 1292 AAGAACGAGCTGAGATCAGGCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 1351
 Db 1021 AAGAACGAGCTGAGATCAGGCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
 Qy 1352 CCAATATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1411
 Db 1081 CCAATATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1340
 Qy 1412 CACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1471
 Db 1141 CACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
 Qy 1472 AGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1531
 Db 1201 AGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
 Qy 1532 GCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1591
 Db 1261 GCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
 Qy 1592 TCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1651
 Db 1321 TCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
 Qy 1652 GCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1711
 Db 1381 GCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
 Qy 1712 ACACAGAGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1771
 Db 1441 ACACAGAGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
 Qy 1772 ATGCTGCTGAG 1831
 Db 1501 ATGCTGCTGAG 1560
 Qy 1832 AGCTGCTGAG 1891
 Db 1561 AGCTGCTGAG 1620

[illegible][illegible][illegible][illegible]

[illegible]

; PRIOR APPLICATION NUMBER: JP 2001-328381
 ; PRIOR FILING DATE: 2001-09-14
 ; NUMBER OF SEQ ID NOS: 3181
 ; SOURCE: GenBank Ver. 2.1
 ; SEQ ID NO 673
 ; LENGTH: 2102
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-094-749-673

Query Match 52.9%; Score 1762.4; DB 16; Length 2102;
 Best Local Similarity 92.2%; Pred. No. 0;
 Matches 1537; Conservative 0; Mismatches 1; Indels 164; Gaps 1;

507 TACATCATCTGTGGCAAAATTAAGAGAGAGAGTGGGAAAGAGGACTTATTGTGTATGCG 566
 Db 1 TACATCATCTGTGGCAAAATTAAGAGAGAGTGGGAAAGAGGACTTATTGTGTATGCG 60
 567 CATCATCTGTGGCAAAATTAAGAGAGAGTGGGAAAGAGGACTTATTGTGTATGCG 626
 Db 1 CATCATCTGTGGCAAAATTAAGAGAGAGTGGGAAAGAGGACTTATTGTGTATGCG 120
 61 CCAATGATGATGTGAATCTCAATTTGATGAGCGGCTATTGTGAATACATACATCCCAT 120
 Db 61 CCAATGATGATGTGAATCTCAATTTGATGAGCGGCTATTGTGAATACATACATCCCAT 120
 627 AACGGAAGAAGTGTCTGTAATGATGAGCGGCTATTGTGAATACATACATCCCAT 686
 Db 627 AACGGAAGAAGTGTCTGTAATGATGAGCGGCTATTGTGAATACATACATCCCAT 686
 121 AACGGAAGAAGTGTCTGTAATGATGAGCGGCTATTGTGAATACATACATCCCAT 180
 Db 121 AACGGAAGAAGTGTCTGTAATGATGAGCGGCTATTGTGAATACATACATCCCAT 180
 687 TTTCGAGCGCTATTAATGATGAGCGGCTATTGTGAATACATACATCCCAT 746
 Db 687 TTTCGAGCGCTATTAATGATGAGCGGCTATTGTGAATACATACATCCCAT 746
 181 TTTCGAGCGCTATTAATGATGAGCGGCTATTGTGAATACATACATCCCAT 240
 Db 181 TTTCGAGCGCTATTAATGATGAGCGGCTATTGTGAATACATACATCCCAT 240
 747 AGTGTAAATTAAGAGCTCATGAGATCAGCGAAATTAAGTGTGATGATTCAG 806
 Db 747 AGTGTAAATTAAGAGCTCATGAGATCAGCGAAATTAAGTGTGATGATTCAG 806
 241 AGTGTAAATTAAGAGCTCATGAGATCAGCGAAATTAAGTGTGATGATTCAG 300
 Db 241 AGTGTAAATTAAGAGCTCATGAGATCAGCGAAATTAAGTGTGATGATTCAG 300
 807 TCAGAAAGTGTAGTGTAGATCAAGAGCTCCCAAGATGTGCTCTCTCTTCAAGCTG 866
 Db 807 TCAGAAAGTGTAGTGTAGATCAAGAGCTCCCAAGATGTGCTCTCTCTTCAAGCTG 866
 301 TCAGAAAGTGTAGTGTAGATCAAGAGCTCCCAAGATGTGCTCTCTCTTCAAGCTG 360
 Db 301 TCAGAAAGTGTAGTGTAGATCAAGAGCTCCCAAGATGTGCTCTCTCTTCAAGCTG 360
 867 TTTTCTCACTGCTACTCTGGTAAATCGAGAGAGCTTCAACTCTGTCACCTGCTGC 926
 Db 867 TTTTCTCACTGCTACTCTGGTAAATCGAGAGAGCTTCAACTCTGTCACCTGCTGC 926
 361 TTTTCTCACTGCTACTCTGGTAAATCGAGAGAGCTTCAACTCTGTCACCTGCTGC 420
 Db 361 TTTTCTCACTGCTACTCTGGTAAATCGAGAGAGCTTCAACTCTGTCACCTGCTGC 420
 927 ----- 926
 Db 927 ----- 926
 431 AGGTGGGTTTCTGAGTCTCTGTTGTTTCCCTGGCTCTCTGGAAGAAATTCACCTCT 480
 Db 431 AGGTGGGTTTCTGAGTCTCTGTTGTTTCCCTGGCTCTCTGGAAGAAATTCACCTCT 480
 927 ----- 926
 Db 927 ----- 926
 481 AGTCCCTATCTGCATCTCTCCGCTCTGCTTACTGTGCGAAATTCGGCAACCTAAT 540
 Db 481 AGTCCCTATCTGCATCTCTCCGCTCTGCTTACTGTGCGAAATTCGGCAACCTAAT 540
 927 ----- AGCAGTATGTCAGCT 942
 Db 927 ----- AGCAGTATGTCAGCT 942
 541 TCTTCCCAATCTTATCTGCTGCTCGAGCGAGATGCTTCAACAGAGAGCTGATGACGA 600
 Db 541 TCTTCCCAATCTTATCTGCTGCTCGAGCGAGATGCTTCAACAGAGAGCTGATGACGA 600
 943 GATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1002
 Db 943 GATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1002
 601 GATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1060
 Db 601 GATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1060
 1003 CGAGCTCATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1062
 Db 1003 CGAGCTCATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1062
 661 CGAGCTCATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
 Db 661 CGAGCTCATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
 1063 GTTGGCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1122
 Db 1063 GTTGGCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1122
 721 GTTGGCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 780
 Db 721 GTTGGCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 780
 1123 GCACTGTAGTGGGATCTCCGCTCGGCAACATGCTTACCTGCTACATGATGATGATG 1182
 Db 1123 GCACTGTAGTGGGATCTCCGCTCGGCAACATGCTTACCTGCTACATGATGATGATG 1182
 781 GCACTGTAGTGGGATCTCCGCTCGGCAACATGCTTACCTGCTACATGATGATGATG 840
 Db 781 GCACTGTAGTGGGATCTCCGCTCGGCAACATGCTTACCTGCTACATGATGATGATG 840
 1183 GATGACATGCTTTAGTGAAGCTTACAGATTTGTGAAGGAAGAAAGACCTATATATC 1242
 Db 1183 GATGACATGCTTTAGTGAAGCTTACAGATTTGTGAAGGAAGAAAGACCTATATATC 1242

1243 TCACACCTCAATTTTCTGGCCCAACTCTGCACTATGAGAGAGATTAAGACACGAGC 1302
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 901 TCACACCTCAATTTTCTGGCCCAACTCTGCACTATGAGAGAGATTAAGACACGAGC 960
 Db 901 TCACACCTCAATTTTCTGGCCCAACTCTGCACTATGAGAGAGATTAAGACACGAGC 960
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 Db 1303 TGGAGCATCAGGCGCAAGAGCAAACTCAAGCTGTCTGCACTGAGAGAGCAATTAAGAC 1020
 961 TGGAGCATCAGGCGCAAGAGCAAACTCAAGCTGTCTGCACTGAGAGAGCAATTAAGAC 1020
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 1363 TGTCTCTGCTCTCTCAGAGAGTGGACAGAAAAAGAGAGCGCTCTCACTGCAACCTCTGTC 1422
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 1021 TGTCTCTGCTCTCTCAGAGAGTGGACAGAAAAAGAGAGCGCTCTCACTGCAACCTCTGTC 1080
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 1423 CGACTCTGCTCTCTCAGAGAGTGGACAGAAAAAGAGAGCGCTCTCACTGCAACCTCTGTC 1482
 Db 1423 CGACTCTGCTCTCTCAGAGAGTGGACAGAAAAAGAGAGCGCTCTCACTGCAACCTCTGTC 1080
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 1663 ATCAGAGAGATCTTGGAAATCAACAAAACCTTCTCACTATCTGATGGAGCAACAGCTCT 1722
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 1321 ATCAGAGAGATCTTGGAAATCAACAAAACCTTCTCACTATCTGATGGAGCAACAGCTCT 1380
 Db 1321 ATCAGAGAGATCTTGGAAATCAACAAAACCTTCTCACTATCTGATGGAGCAACAGCTCT 1722
 1723 ATGCGCAAGTCTTCAAGCACTATCGAGAGAGCTCCGAAACAGCTCTCGATGAA 1782
 Db 1723 ATGCGCAAGTCTTCAAGCACTATCGAGAGAGCTCCGAAACAGCTCTCGATGAA 1440
 1381 ATGCGCAAGTCTTCAAGCACTATCGAGAGAGCTCCGAAACAGCTCTCGATGAA 1440
 Db 1381 ATGCGCAAGTCTTCAAGCACTATCGAGAGAGCTCCGAAACAGCTCTCGATGAA 1782
 1783 GAGGAGAGCAGCATCTCCCAAGAGCTGACAGACCGCAAGCGCTTGAGAGAGCAGAGCA 1842
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 1441 GAGGAGAGCAGCATCTCCCAAGAGCTGACAGACCGCAAGCGCTTGAGAGAGCAGAGCA 1500
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 1843 GCGATGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1902
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 Db 1903 ACTGCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1620
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 1963 ACTGCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2022
 Db 1963 ACTGCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1680
 2022 ACTGCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2082
 Db 2022 ACTGCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1740
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 Db 1681 ACTGCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2082
 2083 ACTGCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2142
 Db 2083 ACTGCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1800
 1741 ACTGCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1800
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 2143 ACTGCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2202
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 Db 1860 ACTGCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2202
 2202 ACTGCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2262
 Db 2202 ACTGCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1860
 1861 ACTGCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1860
 Db 1861 ACTGCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2262
 2262 ACTGCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2322
 Db 2262 ACTGCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1920
 1920 ACTGCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1980
 Db 1920 ACTGCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1980

Qy 1313 GGCCGAAGGCAAACTCAAGCTGCTGCACTTGGAGAGCCAAATGAAGCTGTCCTCT 1372
 Db 1311 TGGAGAGAGAGCACTTGGAGAGCCAAATGAAGCTGTCCTCTCTTCTGTCGAAATAT 2160
 Qy 1371 GGCCGAAGGCAAACTCAAGCTGCTGCACTTGGAGAGCCAAATGAAGCTGTCCTCT 1080
 Qy 1373 GTCTCGAAGAGGCTGGAAGAGCAAGAGCCGCTGATCGAGCTGTCGAGCTGCTCT 1432
 Db 1371 GTCTCGAAGAGGCTGGAAGAGCAAGAGCCGCTGATCGAGCTGTCGAGCTGCTCT 2492
 Db 1081 GTCTCGAAGAGGCTGGAAGAGCAAGAGCCGCTGATCGAGCTGTCGAGCTGCTCT 1140
 Qy 1433 ACTTCGAGAGGAGAGAGCAAGAGCTGTCGATCGAGCTGTCGAGCTGTCGAGCT 1482
 Db 1141 ACTTCGAGAGGAGAGAGCAAGAGCTGTCGATCGAGCTGTCGAGCTGTCGAGCT 1200
 Qy 1491 GTTCGAGAGGCTGTCGATCGAGAGCAAGAGCTGTCGATCGAGCTGTCGAGCTG 1552
 Db 1201 GTTCGAGAGGCTGTCGATCGAGAGCAAGAGCTGTCGATCGAGCTGTCGAGCTG 1260
 Qy 1553 TCCGAGAGGCTGTCGATCGAGAGCAAGAGCTGTCGATCGAGCTGTCGATCGA 1612
 Db 1261 TCCGAGAGGCTGTCGATCGAGAGCAAGAGCTGTCGATCGAGCTGTCGATCGA 1320
 Qy 1613 TCAGTTTATATTCAGAGCAGTCGAGAGCTGTCGATCGAGCTGTCGATCGA 1672
 Db 1321 TCAGTTTATATTCAGAGCAGTCGAGAGCTGTCGATCGAGCTGTCGATCGA 1380
 Qy 1673 GCTTTGGAATATACAGAGCTGTCGATCGAGCTGTCGATCGAGCTGTCGATCG 1732
 Db 1381 GCTTTGGAATATACAGAGCTGTCGATCGAGCTGTCGATCGAGCTGTCGATCG 1440
 Qy 1733 TCCGCTGTTTACAGAGCTGTCGAGAGCTGTCGAGAGCTGTCGAGAGCTGTCG 1792
 Db 1441 TCCGCTGTTTACAGAGCTGTCGAGAGCTGTCGAGAGCTGTCGAGAGCTGTCG 1500
 Qy 1793 TCCGCTGTTTACAGAGCTGTCGAGAGCTGTCGAGAGCTGTCGAGAGCTGTCG 1852
 Db 1501 TCCGCTGTTTACAGAGCTGTCGAGAGCTGTCGAGAGCTGTCGAGAGCTGTCG 1560
 Qy 1853 TCGTGAAGTACAGAGCTGTCGAGAGCTGTCGAGAGCTGTCGAGAGCTGTCG 1912
 Db 1561 TCGTGAAGTACAGAGCTGTCGAGAGCTGTCGAGAGCTGTCGAGAGCTGTCG 1620
 Qy 1913 AGTCGAGAGCTGTCGAGAGCTGTCGAGAGCTGTCGAGAGCTGTCGAGAGCTG 1972
 Db 1621 AGTCGAGAGCTGTCGAGAGCTGTCGAGAGCTGTCGAGAGCTGTCGAGAGCTG 1680
 Qy 1973 CAGCAGCTGTCGAGAGCTGTCGAGAGCTGTCGAGAGCTGTCGAGAGCTGTCG 2032
 Db 1681 CAGCAGCTGTCGAGAGCTGTCGAGAGCTGTCGAGAGCTGTCGAGAGCTGTCG 1740
 Qy 2033 CCGCAGAGCTGTCGAGAGCTGTCGAGAGCTGTCGAGAGCTGTCGAGAGCTG 2092
 Db 1741 CCGCAGAGCTGTCGAGAGCTGTCGAGAGCTGTCGAGAGCTGTCGAGAGCTGTCG 1800
 Qy 2093 TTCTCATGCTGTCGAGAGCTGTCGAGAGCTGTCGAGAGCTGTCGAGAGCTGTCG 2152
 Db 1801 TTCTCATGCTGTCGAGAGCTGTCGAGAGCTGTCGAGAGCTGTCGAGAGCTGTCG 1860
 Qy 2153 CAGTCGCTGTCGAGAGCTGTCGAGAGCTGTCGAGAGCTGTCGAGAGCTGTCG 2212
 Db 1861 CAGTCGCTGTCGAGAGCTGTCGAGAGCTGTCGAGAGCTGTCGAGAGCTGTCG 1920
 Qy 2213 AAGTCGATGTCGAGAGCTGTCGAGAGCTGTCGAGAGCTGTCGAGAGCTGTCG 2272
 Db 1921 AAGTCGATGTCGAGAGCTGTCGAGAGCTGTCGAGAGCTGTCGAGAGCTGTCG 1980
 Qy 2273 AAGTCGATGTCGAGAGCTGTCGAGAGCTGTCGAGAGCTGTCGAGAGCTGTCG 2332
 Db 1981 AAGTCGATGTCGAGAGCTGTCGAGAGCTGTCGAGAGCTGTCGAGAGCTGTCG 2040
 Qy 2333 CTGGGAGAGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 2392
 Db 2041 CTGGGAGAGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 2100
 Qy 2393 TGAGAGAGAGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 2452

RESULT 15

US-10-072-012-257
 Sequence 257 Application US/10072012

Publication No. US20040031493A1

GENERAL INFORMATION:

APPLICANT: Tchernov, Velizar
 INVENTOR: Tchernov, Velizar
 APPLICANT: Zetruksen, Bryan
 INVENTOR: Zetruksen, Bryan
 APPLICANT: Pattusujan, Meera
 INVENTOR: Shinkete, Richard
 APPLICANT: Gai, Lili
 INVENTOR: Gai, Lili
 APPLICANT: Pedgaris, Muralidhara
 INVENTOR: Anderson, David W.
 APPLICANT: Rastelli, Luca
 INVENTOR: Rastelli, Luca
 APPLICANT: Miller, Charles E.
 INVENTOR: Miller, Charles E.
 APPLICANT: Tausip Jr, Raymond J.
 INVENTOR: Gusev, Vladimir Y.
 APPLICANT: Colman, Steven D.
 INVENTOR: Colman, Steven D.
 APPLICANT: Penne, Carol E.
 INVENTOR: Penne, Carol E.
 APPLICANT: Purkay, Katarzyna
 INVENTOR: Grosse, William M.
 APPLICANT: Alsobrook II, John P.
 INVENTOR: Alsobrook II, John P.
 APPLICANT: Rieser, Daniel K.
 INVENTOR: Rieser, Daniel K.
 APPLICANT: Burgess, Catherine E.
 INVENTOR: Burgess, Catherine E.
 TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
 CITE REFERENCE: 21402258 US/10/072,012
 CURRENT FILING DATE: 2002-01-31
 PRIOR APPLICATION NUMBER: 60/265,102
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: 60/265,514
 PRIOR FILING DATE: 2001-01-31
 PRIOR APPLICATION NUMBER: 60/265,517
 PRIOR FILING DATE: 2001-01-31
 PRIOR APPLICATION NUMBER: 60/265,412
 PRIOR FILING DATE: 2001-01-31
 PRIOR APPLICATION NUMBER: 60/265,395
 PRIOR FILING DATE: 2001-01-31
 PRIOR APPLICATION NUMBER: 60/266,406
 PRIOR FILING DATE: 2001-02-07
 PRIOR APPLICATION NUMBER: 60/266,767
 PRIOR FILING DATE: 2001-02-07
 PRIOR APPLICATION NUMBER: 60/267,057
 PRIOR FILING DATE: 2001-02-07
 PRIOR APPLICATION NUMBER: 60/266,975
 PRIOR FILING DATE: 2001-02-07
 PRIOR APPLICATION NUMBER: 60/267,459
 PRIOR FILING DATE: 2001-02-08
 Remaining Prior Application data removed - See File Wrapper or PALM.
 Software: PatentLin Ver. 2.1

SEQ ID NO 257

LENGTH: 2071

TYPE: DNA

US-10-072-012-257

US-10-072-012-257

US-10-072-012-257

US-10-072-012-257

US-10-072-012-257

US-10-072-012-257

US-10-072-012-257

US-10-072-012-257

Query Match 51.4% Score 1712.4; DB 13; Length 2071;
 Best Local Similarity 51.6% P-Value 1.1e-13; DB 13;
 Matches 1396; Conservative 0; Mismatches 2;

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Db 341 GCTCAACTCTCTTCACTGCTGCA-GGTGGTTTGTCTAGTTCTCTGTTTCTCT 399
 Qy 29 ----- 29
 Db 400 GGCCTCTGTGAAGAAACCACTCTAGTCTCTACTCTGCATTTCTGAGCTTCTACT 459
 Qy 29 ----- 29
 Db 460 GTTCCCAACTGTGSCCAACACCAATTTCTCCAACTTTATCTGTGCTGCAGAGAT 519
 Qy 30 ----- GluLeuMergdInhAndyIledIyVrVaLeuAenAserAen 45
 Db 520 GTTCTCAACAGAGACTCTGCGAGATGGAGTGGATATGTATGTATATCTCCAGAT 579
 Qy 46 ThrCysProIysProApheIleProGluSerHisPheLeuAlaProValAenAen 65
 Db 580 ACTGTCTCAACAGACTCTTATCTCCCAAGTCTCATTTCTGCTGTGCTGTGATGAC 639
 Qy 66 SerPheCysGluLeuValLeuProTrpLeuApsPheValAenAenAenAen 85
 Db 640 AGCTTTGTGGAATTTTCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 699
 Qy 86 LysAlaSerAenGlyCysValLeuValHisCysLeuAenAenAenAenAenAen 105
 Db 700 AAAGCTCTCAACAGATGTCTGTAGTGCATCTCTTAGTGGAGTCTCCGCTCGCAC 759
 Qy 106 IleAlaIleAlaPheIleCysValGluSerPheSerLeuAenAenAenAenAen 125
 Db 760 ATGCTGTCTGTCTACATCAAGAGATGAGATGCTCTTAGTGAAGCTTACAGATTT 145
 Qy 126 ValIysGluLeuValPheProHisSerProAenPheAenAenAenAenAenAen 145
 Db 820 GTGAAGAGAAAGAGACTACTATCTCCAACTCTCAATTTCTGTCACATCTCTGAC 879
 Qy 146 ThrCysIleValIleAenAenAenAenAenAenAenAenAenAenAenAenAen 165
 Db 880 TATGAGAGAGATGAGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 939
 Qy 166 LeuIleAenAenAenAenAenAenAenAenAenAenAenAenAenAenAenAen 185
 Db 940 CTGCTGTGAGAGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 999
 Qy 186 GluThrProLeuSerProTrpCysAlaAenAenAenAenAenAenAenAenAenAen 205
 Db 1000 GAGAGCTCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1059
 Qy 206 ProValIleAenAenAenAenAenAenAenAenAenAenAenAenAenAenAen 225
 Db 1060 CCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1119
 Qy 226 SerProLeuValGluAenAenAenAenAenAenAenAenAenAenAenAenAen 245
 Db 1120 AGCTCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1179
 Qy 246 AenAenAenAenAenAenAenAenAenAenAenAenAenAenAenAenAenAen 265
 Db 1180 AATAGCTCAGAGCT 1239
 Qy 266 AlaAlaSerAenAenAenAenAenAenAenAenAenAenAenAenAenAenAen 285
 Db 1240 GAGAGCT 1299
 Qy 286 ThrThrLeuAenAenAenAenAenAenAenAenAenAenAenAenAenAenAen 305
 Db 1300 ACTACTCTGTGAGAGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 1359
 Qy 306 GluThrProLeuThrSerProAenAenAenAenAenAenAenAenAenAenAenAen 325
 Db 1360 CAGCTCTGAGAGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 1419
 Qy 326 AlaAenAenAenAenAenAenAenAenAenAenAenAenAenAenAenAenAen 345

Db 1420 GCGAGCTTCAACAGAGAGAGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 1479
 Qy 346 ThrAlaGluAenAenAenAenAenAenAenAenAenAenAenAenAenAenAenAen 365
 Db 1480 ACCCTGAGAGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 1539
 Qy 366 HisThrSerPheLeuPheGlyLeuSerThrGlnGluHisLeuThrIleValAenAen 385
 Db 1540 CACACAGCT 1599
 Qy 386 LeuGlyLeuValGlyTrpPheAenAenAenAenAenAenAenAenAenAenAenAen 405
 Db 1600 CTGAGCTTCAACAGAGAGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 1659
 Qy 406 ThrSerSerTrpPheAlaThrGluSerSerHisPheAenAenAenAenAenAenAen 425
 Db 1660 ACACAGAGCTGTGATTTGCGACAGAGATCTCTCACTCTCTCTCTCTCTCTCTCTCTCT 1719
 Qy 426 GluGlyGluAenAenAenAenAenAenAenAenAenAenAenAenAenAenAenAen 445
 Db 1720 GAGAGAGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 1779
 Qy 446 ValCysGluThrGluAenAenAenAenAenAenAenAenAenAenAenAenAenAen 465
 Db 1780 GTTATCTCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1839
 Qy 466 HisGluGluSerProPheGluLeuAenAenAenAenAenAenAenAenAenAenAenAen 485
 Db 1840 CATGAGAGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 1899
 Qy 486 GluSerIleAenAenAenAenAenAenAenAenAenAenAenAenAenAenAenAen 505
 Db 1900 GAGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 1959
 Qy 506 SerPheSerGlySerMetGluIleAenAenAenAenAenAenAenAenAenAenAen 517
 Db 1960 AGCTTTTCTGAGAGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 1995

RESULT 2
 US-09-816-494-1
 ; Sequence 1, Application US/09816494
 ; INVENTOR: MEYER, RACHEL A.
 ; APPLICANT: MEYER, RACHEL A.
 ; TITLE OF INVENTION: 38592 AND 21117, NOVEL DUAL SPECIFICITY
 ; TITLE OF INVENTION: PHOSPHATE MOLECULES AND USES THEREFOR
 ; CURRENT APPLICATION NUMBER: US/09/816,494
 ; PRIOR FILING DATE: 2001-03-23
 ; PRIOR APPLICATION NUMBER: US 60/191,858
 ; PRIOR FILING DATE: 2000-03-24
 ; SOFTWARE: PARASO for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 3544
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (589)...(2583)
 US-09-816-494-1

Alignment Scores:
 Pred. No.: 1,116-253 Length: 3544
 Score: 2606.00 Matches: 516
 Best Local Similarity: 90.21% Identical: 1
 Query Match: 97.68% Indels: 56
 DB: 4 Gaps: 1

US-09-964-277-21 (1-517) X US-09-816-494-1 (1-3544)
 Qy 1 McLeuProLeuSerGluInThrValAenAenAenAenAenAenAenAenAenAenAenAen 20

869 AGTGGCCCTCTCTCTGAGACGTTTCTCTCATCTACTCTCTGGGTAACTGAGAGCA 328
21 AAlaSerThrLeuPheHisCysLeuGln----- 29
929 GCTTCACTCTGTTCACTCTCTCTCA-----GTTGGTGTCTGGATGCTCTCTGTTTCCCT 987
29 ----- 29
988 GGCTCTGTGTGAAGAAATCACTCTAGTCCCTACCTGCATTTCTCAGCTCTCTACT 1047
29 ----- 29
1048 GTTGTCCACANTGTGGCCCAACCCGAGATTTCTCCCACTCTTTATCTTGGTGGCAGCGAGAT 1107
30 -----GluLeuSerGluGlyIleAspGlyIleGlyGlyValLeuLeuAlaSerAsn 45
1108 GTTCTCCAGCAGAGCACTGATCGACGAGANTGGATGTTGTATGTGTAATGTCCAGCAAT 1167
65 SerProGlySerProAspPheIleProIleuSerIlePheIleAspGlyValValLeuAsp 155
1166 ACTCTTCGAAAGCTGACTTTCTCTCCGCTGCTCATTTCTCTGCTGTGGCTGTGATGATGAC 1227
66 SerPheCysGluIleuGlyIleuProIleuPheAspIleuSerValAlaPheIleuGlyIleuAla 85
1228 AACTTTTGTGAAATATTTTGTGGTGTGGACATGCTGACATGCTGATTTCTGTGGAGAGCA 1287
86 LysAlaSerAspGlyCysValLeuValIleHisCysGluAlaGlyIleSerAspSerAlaThr 105
1288 AAGCTCTCCAGAGATGATGTTGTATGGTCACTTCTCTGAGTCTCCCTCTGCCCTCACC 1347
106 AlaLeuAlaLeuIleuGlyIleuGlyIleuGlyIleuGlyIleuGlyIleuGlyIleuGlyIleu 125
1348 ATGCTGCTATGCTCATCTGTCGAGAGAGAGTGGAGATGTTCTTTAGATGAGCTTACAGATT 1407
126 ValIleuGlyIleuGlyProThrIleuSerProAspPheAsnPheLeuGlyIleuLeuAsp 145
1408 GTGGAGAGAAAGAGACATCTATCTCTCCAACTCTCAATTTCTGGGGCAGCTCTCGGAC 1467
146 GCTGlyIleuGlyIleuGlyIleuGlyIleuGlyIleuGlyIleuGlyIleuGlyIleuGlyIleu 155
1468 TATGAGAGAGAGATATAGAGACACGAGCTGGAGCATCAAGGCGCAAGAGCAACCTCAAGCTG 1527
166 LeuIleuGluIleuGlyProIleuGlyIleuProAlaValIleuIleuGlyIleuGlyIleuSer 185
1528 CTGGCTCTGGAGAGAGCAATATGACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1587
186 GluThrProLeuSerProProCysAlaAspSerAlaThrSerIleuGluAlaGlyIleuGlyIleu 205
1588 GAGACCTCTCTAGTCTCCCTCTGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1647
206 ProValIleuProAlaLeuProSerValProSerValGlnProSerIleuGlyIleuGlyIleu 225
1648 CCGCTGTCATCCGCGCAGCTGCTCCACAGCTGCCCGAGCTGTCAGCTCTCTCTCTCTCTCT 1707
226 SerProIleuValGluAlaLeuSerIleuGlyIleuSerAlaAspGluIleuGlyIleuSer 245
1708 AGACCCCTGGTATCAAGGGCTGAGTGGGGTGGACCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1767
246 AntGlyIleuGlyIleuGlyIleuGlyIleuGlyIleuGlyIleuGlyIleuGlyIleuGlyIleu 265
1768 ATATAGCTCCAGAGCTGCT 1827
266 AlaAlaSerIleuGlyIleuGlyIleuGlyIleuGlyIleuGlyIleuGlyIleuGlyIleuGlyIleu 285
1828 GAGACCT 1887
286 ThrIleuLeuAspGlyIleuThrIleuValIleuGlyIleuGlyIleuGlyIleuGlyIleuGlyIleu 305
1908 ACTACTCTGTGAG 328
306 GlnThrProGlyIleuSerProAspGlyIleuGluAlaSerIleuGlyIleuGlyIleuGlyIleu 325

[illegible]

RESULT 3
UC-09-030-CCO-3

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; Sequence 3, A
; Patent No. 64
; GENERAL INFORMATION
; APPLICANT: L
; APPLICANT: I
; TITLE OF INVENTION
; FILE REFERENCE
; CURRENT APPLICANT
; CURRENT FILING
;

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; SEQ ID NO: 3
; LENGTH: 2377
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: CD
; LOCATION: (1
US-09-920-668-3

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Alignment Scores:			
Pred. No.:	3.4e-75	Length:	2377
Score:	84.00	Matches:	216
Percent Similarity:	52.9%	Conservative:	59
Best Local Similarity:	41.6%	Mismatches:	142
Query Match:	31.6%	Indels:	102
	4	Gaps:	19

US-09-964-277-21 (1-517) X US-09-920-668-3 (1-2377)


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Alignment Scores:
Pred. No.: 1,964-19 Length: 1238
Score: 289.50 Matches: 72
Percent Similarity: 54.15% Conservative: 39
Query Match: 10.85% Indels: 25
DB: 4 Gaps: 6

US-09-964-277-21 (1-517) X US-09-736-457-803 (1-1238)
QY 29 GInduLeuMeGInduAndgYllegYrValLeuAnaLaserAerhthCysPro 48
Db 693 AGAGACATCTCGGAGCCCTGGGACATCAAGCTCTGTGATGTCTCTCGAGCTGCCA 752
QY 49 LysProAphPheProLusSerHisPheAerGValProValAuaAmpSerPheCys 68
Db 763 AAC--CACTTTGAGGACATCTCAGTACAGATGCATCCAGTGAAGATACACAG 809
QY 69 GluLysPheProLusSerHisPheAerGValProValAuaAmpSerPheCys 88
Db 810 GCCACATCACTCTGTCTGTCAGGACATGAGTACATGATCCGTGAGGCTGC 929
QY 89 AendGlyValLeuHiCysLeuAlaHicSerPheValGlyLeuAlaHicSerPhe 108
Db 870 CTTGGGCGTCTGTCTGTCAGGACATGAGTACATGATCCGTGAGGCTGC 929
QY 109 AlatyPheLeuAerMetPheMetSerLeuAerMetSerLeuAerMetSerLeu 128
Db 930 GCTACTCTGATGAGAACCGGTGAGTCTGAGGAGCTGCTAGC 989
QY 129 LysArgProthPheSerProAerPheAnPheLeuGlyGlyGlyLeuAerPheGly 148
Db 1089 ----CCCTGGAGACCTCTG--GGGAGCGGCGAGAGCCCC 1124
QY 189 LeuSerProCysAlaAerPheAlaHicSerPheValGlyGlyGlyLeuAer 208
Db 1125 GCACACCCC-----ACCTCGAGTTGTCTTCAGCTTTCGGCTC 1163
QY 209 ProAerValProSerValGlnProSerLeuGlnProSerLeuGlnProSer 228
Db 1164 TCGGTGGGCGTCACTCGGCCCCGAGCGCTGCTCTACTCTG--CACAGCCGCTC 1217
QY 229 ValGlnAlaLeuSer 233
Db 1218 AACACCTCTCCGAGC 1232

RESULT 8
US-09-614-1248-003
; Sequence 803
; Patent No. 6667154
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangor, Chaitanya S.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Metter, Marc
; APPLICANT: Metter, Marc
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.478C9
; CURRENT FILING DATE: 2001-07-11
; NUMBER OF SEQ ID NOS: 1668

US-09-614-1248-003
; Sequence 803
; Patent No. 6667154
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangor, Chaitanya S.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Metter, Marc
; APPLICANT: Metter, Marc
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.478C9
; CURRENT FILING DATE: 2001-07-11
; NUMBER OF SEQ ID NOS: 1668

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Db      1218  ACCACTCTCCAGC 1232
RESULT 10
US-09-702-705-801
US-09-702-705-801 Application US/09702705
; Patient No. 6504010
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Fanger, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478015
; CURRENT APPLICATION NUMBER: US/09/702,705
; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 1833
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 801
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-702-705-801
Alignment Scores:
Pred. No.: 5,686-19 Length: 1619
Score: 287.00 Matches: 73
Percent Similarity: 55.02% Conservative: 42
Best Local Similarity: 34.93% Mismatches: 69
Query Match: 10.76% Gaps: 6
DB: 4
US-09-964-277-21 (1-517) x US-09-702-705-801 (1-1619)
Qy      29  GlnGluLeuMetGlnGlnGlyLeuValLeuAlaSerAnthrCysPro 48
Db      365  AAGACATCTCGAGCGCCCTGGGATCAAGCTCTGTGAATGTCCTCGAGACTGCCA 424
Qy      49  LysProAlaPhePheProGlnSerHisPheLeuAlaGlyValProValAlaAspSerPheCys 68
Db      425  AAC---CACTTTTGAAGAGCATCTAGTACATGATCCATCCAGTGAAGATACCCACAG 481
Qy      69  GluLysLeuLeuProTTPleuAlaPheSerValAlaPhePheLeuLysValAlaLysAlaSer 88
Db      482  GCCGACATCACTCTCTGTTCTGATGAGCGGATAGATAGATCGATCGAGACTGTC 541
Qy      89  AncGlyCysValLeuHisCysGluAlaGlyLeuSerGlnAlaThrLeuAlaLe 108
Db      542  CTTGGCGCGTCTCTGTCATCTGTCAGAGCCATAGATAGATCGATCGTGAAGACTGC 541
Qy      109  AlatyPheLeuMetLysArgMetAspMetSerLeuAlaPheValPheValAlaLysGlu 128
Db      602  CCGGCGAGCTTCTGCGCTTCTGATGAGCGGATAGATAGATCGATCGAGACTGTC 721
Qy      149  LysLeuAlaandLthrGlyAlaSerGlyPheLysSerLysLeuLysLeuLysLeu 168
Db      722  CAGGTGCTGCGCACTCTCTGCTCTGCTGCGGAGCTGCTAGC----- 760
Qy      169  GluLysProAlaandLuproValProAlaValSerGluLysGlyLysSerGluThrPro 188
Db      761  -----CCCTCGGAGCCCTG-----CGGAGCGGAGAGCCCC 796
Qy      189  LeuSer-ProProCysAlaAspSerAlaThr-----SerGluAlaAlaGlyLysArgPro 206
Db      797  GCACCCCTCCCTCCGAGTCTCTTCGATGTTTCGGTCTTCCTGGCGCTCGATCTGGCC 856
Qy      206  oValHisProAlaSerValProSerValProSerValGlnProSerLeuLeuLysGlu 226
Db      857  C-----CGAGAGCTCTCCCTTACTCTGCACAGCCCTCCATCACACCTCTC----- 899
Qy      226  xProLeuValGluAlaLeuSerGly 234
Db      900  -CCAGCTTTTAGAGCGCCCTCGGG 923
RESULT 11
US-09-736-457-801
; Sequence 801, Application US/09736457
; Patient No. 6509448
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodges, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Li
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478015
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 801
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-736-457-801
Alignment Scores:
Pred. No.: 5,686-19 Length: 1619
Score: 287.00 Matches: 73
Percent Similarity: 55.02% Conservative: 42
Best Local Similarity: 34.93% Mismatches: 69
Query Match: 10.76% Gaps: 6
DB: 4
US-09-964-277-21 (1-517) x US-09-736-457-801 (1-1619)
Qy      29  GlnGluLeuMetGlnGlnGlyLeuValLeuAlaSerAnthrCysPro 48
Db      365  AAGACATCTCGAGCGCCCTGGGATCAAGCTCTGTGAATGTCCTCGAGACTGCCA 424
Qy      49  LysProAlaPhePheProGlnSerHisPheLeuAlaGlyValProValAlaAspSerPheCys 68
Db      425  AAC---CACTTTTGAAGAGCATCTAGTACATGATCCATCCAGTGAAGATACCCACAG 481
Qy      69  GluLysLeuLeuProTTPleuAlaPheSerValAlaPhePheLeuLysValAlaLysAlaSer 88
Db      482  GCCGACATCACTCTCTGTTCTGATGAGCGGATAGATAGATCGATCGAGACTGTC 541
Qy      89  AncGlyCysValLeuHisCysGluAlaGlyLeuSerGlnAlaThrLeuAlaLe 108
Db      542  CTTGGCGCGTCTCTGTCATCTGTCAGAGCCATAGATAGATCGATCGTGAAGACTGC 541
Qy      109  AlatyPheLeuMetLysArgMetAspMetSerLeuAlaPheValPheValAlaLysGlu 128
Db      602  CCGGCGAGCTTCTGCGCTTCTGATGAGCGGATAGATAGATCGATCGAGACTGTC 721
Qy      129  LysArgProAlaThrLeuSerProAlaValSerGluLysGlyLysSerGluThrPro 148
Db      662  -----CCCTCGGAGCCCTG-----CGGAGCGGAGAGCCCC 721

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[illegible]

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899      ...CAGGACCCCTTACTCGAAGCCCCCATCAACAATCTTC...
870 C-----CAGGACCCCTTACTCGAAGCCCCCATCAACAATCTTC-----
db          226   rfdonvaldghablaawserucy  214
QY          226   rfdonvaldghablaawserucy  214
DB          900 -CCAGCGTTTAGAGCCGCCCTCGGG    923
            .....|.....|.....|.....|.....|.....|.....|.....|
RESULT 13
RSDU-071-325-901
; Sequence 801, Application US/09671325
; Patent No. 6667154
; GENERAL INFORMATION:
; TITLE OF INVENTION:     DIAGNOSIS AND METHODS FOR THE THERAPY AND PREVENTION OF LUNG CANCER
; APPLICANT:              Rongsheng Long
; APPLICANT:              Bangor, Chaitanya S.
; APPLICANT:              Lodges, Michael A.
; APPLICANT:              Fanger, Gary
; APPLICANT:              Vedrick, Tom
; APPLICANT:              Reiter, Marc
; APPLICANT:              Mannion, Jane
; APPLICANT:              Fan, Liqun
; APPLICANT:              Wang, Yanyan
; TITLE OF INVENTION:     DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE:         210131.478612
; CURRENT APPLICATION NUMBER: US/09/671,325
; PRIORITY CLAIMING DATES: 2005-09-26
; NUMBER OF SEQ NOS.:     905
; SOFTWARE:               FastSeq for Windows Version 3.0
; SEQ ID NO 801
; LENGTH:                 1619
; ORGANISM:               Homo sapiens
US           -09-671-325-901
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Alignment Scores:		5.68e-19	1619
Pred. No.:		Matches:	73
Score:		Mismatches:	10
Percent Similarity:	55.0%	Conservative:	65
Identical Similarity:	10.7%	Indels:	25
Query:		Gaps:	6
DB:	4		

US-09-564-277-21 (1-517) x US-09-671-325-601 (1-1619)	
Qy	29 GlnGLuLewMerGlnGlnGlnGlyLeuYrValLeuAmpLaserAmmThCysPro 48
Db	365 AGRAGCATGTGGAGCGCGTGGAGCATACAGCGCTGTGGATGATCTCTCGAGATGCCA 424
Qy	49 LysProPheAlaPheProGluSerHisPheLeuArgValProValAmpAspSerPheCys 68
Db	425 AACCTTTGAGGACGACTATTCAGACGATCCAGCGCATCCGATCGAGAGTATCAACACAG 481
Qy	69 GluArgLLeuProTrieuAspLysSerValAspPheIleuAluYalAspSer 88

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[illegible][illegible]

RESULT 3

US-10-377-072-27
Sequence 27, Application US/10377072
Publication No. US20040009501A1
GENERAL INFORMATION FOR THE INVENTION
INVENTOR: WILLIAM PHARMACEUTICALS INC.
INVENTOR: CURTIS, RORY A.J.
APPLICANT: LOGAN, THOMAS JOSEPH
APPLICANT: GLUCKSMANN, MARIA A.
APPLICANT: MEYERS, RACHEL E.
APPLICANT: JACOBSON, J.
APPLICANT: RUDOLPH-OWEN, LAURA A.
APPLICANT: CHUN, MIYOUNG
APPLICANT: TSAI, FONG-YING
TITLE OF INVENTION: NOVEL 5-ARYL-2-AMINO-6-ARYL-3,4-DIHYDRO-2H-1,2,4-TRIAZIN-3-ONES AND 5-ARYL-2-AMINO-6-ARYL-3,4-DIHYDRO-2H-1,2,4-TRIAZIN-3-ONE DERIVATIVES
TITLE OF INVENTION: AND USES THEREFOR
FILE REFERENCE: MP103-0180MM
CURRENT APPLICATION NUMBER: US/10/377,072
CURRENT FILING DATE: 2003-08-27
PRIORITY NUMBER: US 09/785,860
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/215,370
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: US 09/723,806
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: US 60/187,455
PRIOR FILING DATE: 2000-03-07
PRIOR APPLICATION NUMBER: US 09/843,297
PRIOR FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: US 60/199,801
PRIOR FILING DATE: 2000-09-04
PRIOR APPLICATION NUMBER: US 09/861,801
PRIOR FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: US 60/205,508

1142 AGCCGCTGGTGTACAGGCGGCTCAGTGGGCTGGCACTCTCTCCGACGACGCTGGAGACAGC 1201
246 AAmlyVdLmlyVdWdSerPhaSerCubAba1TcVdWdSerValSerYdSerAaSerMet 265
1202 AATAAAGTCAAGCGCTCTCTCTCTGGATCAAAATCAGTTTATATATCAACCAAGCATG 1261
266 ThAaSerLmlyVdWdSerPhaSerCubAba1TcVdWdSerValSerYdSerAaSerMet 285
1262 GGAAGATCTCTACATAGGCTCTCTCTCATCAGAGATGTTTGATATCTACAAACCTTCC 1321
286 ThThriaLmlyVdWdSerPhaSerCubAba1TcVdWdSerValSerYdSerAaSerMet 305
1322 ACTACCTGGATGGACGACGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1381
306 GluThrProGluIntrSerProApplpdyGluLmlyVdWdSerValSerYdSerAaSerMet 325
1382 CAGGACGACGATCT 1441
326 AlAaTcProSerAaSerGluIntrSerPhaSerCubAba1TcVdWdSerValSerYdSerAaSerMet 345
1442 GCGAGCTCTCAGACACGACGACGACGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1501
346 ThAaLmlyVdWdSerPhaSerCubAba1TcVdWdSerValSerYdSerAaSerMet 365
1502 ACAGCGCTAGAGTCCCTTTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1561
366 ThAaLmlyVdWdSerPhaSerCubAba1TcVdWdSerValSerYdSerAaSerMet 385
1562 CAACACGCT 1621
386 LmlyVdLmlyVdWdSerPhaSerCubAba1TcVdWdSerValSerYdSerAaSerMet 405
1622 TGGGCTCTAAGCGCTGGCATCTGGATATTTGGGCTCTCTCTCTCTCTCTCTCTCTCTCT 1681
406 ThSerSerTriPrpPhaLmlyVdWdSerPhaSerCubAba1TcVdWdSerValSerYdSerAaSerMet 425
1682 ACAGGACGATCT 1741
426 GtGVdSerAaSerValSerYdSerCubAba1TcVdWdSerValSerYdSerAaSerMet 445
1742 GAGGACGATCT 1801
446 ValTySerValAaSerGluIntrSerProApplpdyGluLmlyVdWdSerValSerYdSerAaSerMet 465
1802 CTATATCT 1861
466 ThAaLmlyVdWdSerPhaSerCubAba1TcVdWdSerValSerYdSerAaSerMet 485
1862 CATGAG 1921
486 GluSerLmlyVdWdSerPhaSerCubAba1TcVdWdSerValSerYdSerAaSerMet 505
1922 GAGACGATCT 1981
506 SerPhaSerGluIntrSerProApplpdyGluLmlyVdWdSerValSerYdSerAaSerMet 517
1982 AGGCT 2017

RESULT a

3-10-257-026-1

Sequence 1, Application US/10257026

Publication No. US20040086859A1

GENERAL INFORMATION:

APPLICANT: Merck Patent GmbH

TITLE OF INVENTION: New dual specificity phosphatase

FILE REFERENCE: DUSP10KDWS

CURRENT APPLICATION NUMBER: US/10/257,026

CURRENT PILING DATE: 2003-11-07

NUMBER OF SEQ ID NOS: 3

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1

LENGTH: 3059

10

100

TYPE: DNA	1,166,259	Length:	3059
ORGANISM: Homo sapiens	260,600	Mismatch:	548
NAME/ACC: U01101	Percent Similarity: 90.21%	Conservative:	0
NAME/REV: U01101	Percent Local Similarity: 90.21%	Mismatches:	1
LOCATION: (127)..(2121)	Percent Match: 17.68%	Gaps:	16
US-10-257-026-1	DB:		1
Alignment Scores:			
Score: 1,166,259			
Score: 260,600			
Score: 90.21%			
Score: 90.21%			
Score: 17.68%			
Score: 1			

US-09-964-277-2; (1-517) x US-10-257-026-1 (1-3059)

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206 proValHisProIleSerValProSerValGlnProSerLeuIleuLysP
Oy 225
1186 CCCGTGCATCCGCCAGCTGGCCAGCTGCCCAGCGTCCCTGTTCACGAC 1214S
DD

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Qy 226 SerProLeuValGlnAlaLeuSerGlyValuHisLeuSerAlaAlaProGlyLeuGluAspSer 245
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Qy 246 AlanProValGlnGlySerPheSerLeuAlaGlySerGlySerGlySerGlySerGlyMet 265
Db 1306 AATAGAGCTGAAGGCTTCCTCTCTCTGGATATCAATACAGTCTCATATTCGAGAGGATG 1365
Qy 266 AlaAlaSerLeuGlyPheSerSerSerGlyAlaAlaLeuGlnGlyTyrosylProSer 285
Db 1366 GAGGATCTCTAGATAGCTCTCTCTCATGAGAGAGTCTTCGATCTACAGAGCTCTCC 1425
Qy 286 ThrThrLeuLeuGlyThrAlaGlyGlnCysGlnPheSerProValGlnGluLeuSerGly 305
Db 1426 ACTACTGATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1485
Qy 306 GlnHisProGlyHisSerProAlaGlyLeuGlyAlaSerPheProValGlyLeuLeuThr 325
Db 1486 CAGATCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1545
Qy 326 AlaArgProSerAlaSerGlyAlaSerGlyHisSerGlyHisSerValArgThrSerSerGly 345
Db 1546 GCGAGCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1605
Qy 346 ThrAlaSerGlyLeuLeuSerProLeuHisAlaSerGlyGlySerValGlnAlaAspGly 365
Db 1606 ACCGCGCGAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1665
Qy 366 HisThrSerPheLeuPheGlyValSerThrSerGlyHisLeuAlaProGlySerGlyAla 385
Db 1666 CAGACAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1725
Qy 386 LeuGlyValGlyGlyGlyPheHisSerGlyHisSerGlyHisSerGlyHisSerGlyHis 405
Db 1726 CTGAGCTCTTAAAGGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1785
Qy 406 ThrSerSerProPheAlaThrGlnLeuSerSerHisPheArgSerAlaSerAlaLeuTy 425
Db 1786 ACAGAGAGCTGATATTTCTCCAGAGCTCTGAGATCTCTCTCTCTCTCTCTCTCTCTCT 1845
Qy 426 GlyGlySerAlaSerGlySerAlaArgSerGlySerGlySerGlySerGlySerGlySer 445
Db 1846 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1905
Qy 446 ValArgSerValArgAlaGlyGlnGlyProSerGlySerGlySerGlySerGlySerGly 465
Db 1906 GCTATCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1965
Qy 466 HisGlnGlySerProPheGlyGlnPheValGlyArgSerGlyGlyMetGlyPheGly 485
Db 1966 CATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2025
Qy 486 GlnSerPheSerGlySerGlySerGlySerGlySerGlySerGlySerGlySerGlySer 505
Db 2026 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2085
Qy 506 SerPheSerGlySerMetGlyAlaLeuGlyLeuLeuSer 517

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RESULT 9
US-09-964-277-1

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; Sequence 1, Application US/09964277
; Patent No. US2002037170A1

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; GENERAL INFORMATION:
; Name: us-09-964-277-1

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; Applicant: Met Bio

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; Title of Invention: DSP-16 DUAL-SPECIFICITY PHOSPHATASE

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; File Reference: 200125.434

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; Current Publication Number: US/09/964,277

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; Number of SEQ ID NOS: 22

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; Software: FastSeq for Windows Version 4.0

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; SEQ ID NO 1

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; Name: DNA

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; ORGANISM: Homo sapiens

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US-09-964-277-1

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Alignment Scores:

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Pred. No.: 1,416-259 Length: 3496

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Score: 2606.00 Matches: 516

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Percent Similarity: 90.21% Conservative: 1

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Query Similarity: 97.21% Mismatches: 1

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Query Match: 36 Gaps: 1

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US-09-964-277-21 (1-517) x US-09-964-277-1 (1-3496)

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Qy 21 AlaSerThrAlaPheThrCysGln 29
Db 902 GCTTCTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 960
Qy 29 ----- 29
Db 961 GGCCTCTGTGAGGAAATCCACTAGTCTCCTACCTGATCTCTGAGCTTCTGAGCTTCTTACT 1020
Qy 29 ----- 29
Db 1021 GTTGCGACATCTGGCCACCGAGATCTTCTCCCATCTTATCTGCTGCTCCGCGAGATF 1080
Qy 30 ----- GluLeuMetGlnGlnGlnGlyValLeuAlaSerAla 45
Db 1081 GTCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
Qy 46 ThrCysProLeuProAlaPheLeuProGlySerHisPheLeuGlyValProValLeuAsp 65
Db 1141 ACCTCTCGAAGCTGAGCTGATTCCTCCGAGTCTCATCTCTCTCTCTCTCTCTCTCTCTCTCT 1200
Qy 66 SerPheCysGlnGlyLeuLeuProThrLeuAspGlySerValAspPheLeuGlyValLeu 85
Db 1201 AGCTTTTTCGAGAAATATTTTCTCCGCTGGTGGAGCAATCATGATAGATTTTATTGAGAA 1260
Qy 86 LysAlaSerGlnGlyCysValLeuValHisCysPheGlyLeuLeuSerGlyAlaThr 135
Db 1261 AAGCTCTCAATGAGTGTCTCTGATGCTGCTCTTCTAGCTGAGATCTCTCTCTCTCTCTCT 1320
Qy 106 GluAlaAlaThrThrLeuMetGlyHisPheAspSerLeuAlaArgPhe 125
Db 1321 ATGCTTATGCTCTATCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
Qy 126 ValGlyGlyAspGlyProThrThrLeuSerProLeuPheGlnGlyLeuLeuAsp 145
Db 1381 GTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
Qy 146 ThrGlyLeuValLeuLeuGlnThrThrValAlaSerGlyProLeuSerGlyLeuLeuLeu 165
Db 1441 ATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
Qy 166 LeuHisLeuGlyLeuProAlaGlnProValProAlaValSerGlyGlyGlyGlyLeuSer 185
Db 1501 GCTCTCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
Qy 186 GlnThrProLeuSerProCysAlaAspSerAlaThrSerGlyAlaAlaGlyGlyAsp 205
Db 1561 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
Qy 206 ProValHisProAlaSerValProSerValGlnProSerLeuGlyLeuLeuLeuLeu 225
Db 1621 CCGGTGATCTCCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680
Qy 226 SerProLeuValGlnAlaLeuSerGlyValuHisLeuSerAlaAlaProGlyLeuGluAsp 245

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1691 AGCCGCTGTTGACAGGCTCTGATGGGCTGCTATGTCGCGAGAGCTGGAGAGC 1740
246 AAmuLysValArgSerPheSerLeuAspPheLysSerValSerLysSerAlaSerMet 265
1741 ATATAGCTCAGGCTGCTCTCTCTGATATCATATGTTTATCTTATCTTATCTTATCT 3000
266 AAlaAlaSerLeuAlaGlyPheSerSerSerGluAlaLeuGluGluGluGluGluGlu 285
1801 GAGCATCTCTATGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1860
286 ThrThrLeuAlaGlyThrAlaLysLeuGluGluGluGluGluGluGluGluGluGlu 305
1861 ACTATCTCTGATGAGCAGCAAGCTATGCTGATGCTCTCTCTCTCTCTCTCTCTCTCT 1920
306 GluThrProGluThrSerProLysPheGluGluAlaSerLeuProLysLeuGluGluThr 325
1921 CAGATCTCCGAGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1980
326 AlaAlaProGluSerAspSerGluSerLysValGluSerValAlaGluThrSerSerGly 345
1991 GCGAGGCTCTTCAAGAGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2040
346 ThrAlaGluAlaSerLeuSerProLysLysLysLysLysLysLysLysLysLysLys 365
2041 ACCGCGCAGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2100
366 HisThrLeuAlaSerGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 385
2101 CAGACAGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2160
386 LeuLysLeuGluGlyThrPheSerAspLysLeuAlaSerGluGluGluGluGluGlu 405
2161 CTGAGCTCTTAAAGGCTGAGCTCTGATATCTGCGCTCTCTCTCTCTCTCTCTCTCT 2220
406 ThrSerSerThrThrPheAlaThrGluGluSerHisPheThrLysSerAlaSerAlaThr 425
2221 ACCGAGATCTGATATTTTCAGAGAGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2280
426 GlyLysAlaSerLysSerAlaThrSerCysSerGluLeuProThrCysGlyAspGln 445
2281 GAGAGAGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2340
446 ValThrSerValArgAlaGluGluLeuProSerAspAlaGluSerAspArgSerTrp 465
2341 GATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2400
466 HisGluLeuLeuProGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 485
2401 CAGTAAAGAGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2460
486 GluSerLysLysSerGluAlaGluSerAspGluGluGluGluGluGluGluGluGlu 505
2461 GAGAGCATCTATCTCAGAGAGAGAGTCTCAGGAGAGAGTCTCAGGAGAGAGTCT 2520
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SEQUENCE 10
US-09-816-494-1
Sequence 1, Application US/09816494
Patent No. US20020034807A1
GENERAL INFORMATION:
Inventor: Rachel A.
TITLE OF INVENTION: NOVEL DUAL SPECIFICITY
TITLE OF INVENTION: PHOSPHATASE MOLECULES AND USES THEREFOR
FILE REFERENCE: 10448-030002
PRIORITY REFERENCE: US/09/816,494
CURRENT FILING DATE: 2001-07-23
PRIORITY FILING DATE: US 60/191,859
PRIORITY FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 10

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SOFTWARE: FastSeq For Windows Version 4.0
SEQUENCE:
LENGTH: 3544
TYPE: DNA
ORGANISM: Homo sapiens
NAME/KEY: CDS
LOCATION: (589)...(2583)
US-09-816-494-1
Alignment Scores:
Score: 1,446-259 Length: 3544
Percent Similarity: 2066.00 Matches: 516
Conservative: 0
Gap Penalties: 90-218 Indels: 56
Query Match: 97.68 Gaps: 1
DB: 9

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US-09-964-277-21 (1-517) x US-09-816-494-1 (1-3544)
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21 AlaSerThrLeuPheThrCysGluGluGluGluGluGluGluGluGluGluGluGlu 28
Qy 929 GCTTCAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 987
Db 29 ----- 29
Qy 988 GAGCTCTGTGTGAAGAAATCACTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1047
Db 29 ----- 29
Qy 1048 GTTCCCAACATTGGGCAACACCGCAATCTTCCCAATCTTATCTTGTGCGCAGCGAG 1107
Db 1108 GTCTCCACAGAGAGCTGATCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1167
46 ThrCysProLeuProAspPheLeuProGluSerHisPheLeuArgValProValLeuSer 65
1168 ACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1227
66 SerPheCysGluLysLeuProThrLeuAspPheSerValAspPheLeuGluAla 85
1228 AGCTTTTTCGAGAAATTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1287
86 LysAlaSerAlaGlyCysValLeuValHisCysLeuAlaGlyLysSerAspSerAlaThr 105
1288 AAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1347
106 IleAlaLeuAlaThrLeuMetLysArgMetAspMetSerLeuGluGluAlaThrArgPhe 125
1348 ATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1407
126 ValLysGluLeuArgProThrLysSerProAlaPheLeuGlyLysLeuLeuSer 145
1408 GTTGAAGAAAGAGCTCTACTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1467
146 ThrGluLysValLysLeuLeuThrGluValSerGluValProLysSerSerLeuSer 165
1468 TATGAGAGAGAGATTAAGACAGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1527
166 LeuHisGluGluLeuProSerGluProValProAlaValSerGluGlyGluGluSer 185
1528 CTGCACTCTGAGAGAGCAAAATGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1587
186 GluThrProSerGluProCysAlaLeuSerAlaThrSerGluAlaAlaGlyGluArg 205
1588 GAGAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1647
206 ProValHisProAlaSerValProSerValProSerValGluInProSerLeuGluSer 225

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[illegible]

Search completed: September 24, 2004, 08:56:43
Job time : 767 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

4 protein - protein search, using sw model

in on: September 23, 2004, 14:18:58 : Search time 53 Seconds
(without alignments)
53.311 Million cell updates/sec

title: US-09-964-277-16

sequence: 52 affect score: 52

1 VRLCAGISRS 10

core label: BLOSUM62

Gapop 10.0, Gapext 0.5

sarched: 1586107 seqs, 282547505 residues 1586107

total number of hits satisfying chosen parameters:

inimum DB seq length: 0

aximum DB seq length: 2000000000

ot-processing: Minimum Watch 0%

Listing first 45 summaries

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2. Genesep2003a4.2

3. Genesep2003a4.3

4. Genesep2003a4.4

5. Genesep2003a4.5

6. Genesep2003a4.6

7. Genesep2003a4.7

8. Genesep2003a4.8

Prod. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	DB ID	Description
1	52	100.0	21	ABR52382	Protein r
2	52	100.0	23	ABR52386	Protein r
3	52	100.0	41	ABR52386	Protein r
4	52	100.0	23	ABR52386	Protein r
5	52	100.0	140	ABR52404	Human EST
6	52	100.0	168	ABR52404	Human MAP
7	52	100.0	170	ABR52404	Human MAP
8	52	100.0	170	ABR52404	Human MAP
9	52	100.0	170	ABR52404	Human MAP
10	52	100.0	170	ABR52404	Human MAP
11	52	100.0	170	ABR52404	Human MAP
12	52	100.0	102	ABR52425	Protein r
13	52	100.0	317	ABR52425	Protein r
14	52	100.0	322	ABR52425	Protein r
15	52	100.0	322	ABR52425	Protein r
16	52	100.0	373	ABR52425	Protein r
17	52	100.0	373	ABR52425	Protein r
18	52	100.0	381	ABR52425	Protein r
19	52	100.0	381	ABR52425	Protein r
20	52	100.0	381	ABR52425	Protein r
21	52	100.0	381	ABR52425	Protein r
22	52	100.0	381	ABR52425	Protein r
23	52	100.0	419	ABR52425	Protein r
24	52	100.0	517	ABR52425	Protein r
25	52	100.0	579	ABR52425	Protein r

ALIGNMENTS

RESULT 1

ABR52406

ID ABR52406 standard; peptide: 23 AA.

XX ABR52406;

DT 19-JUN-2003 (first entry)

XX Peptide relating to the invention SEQ ID NO: 144.

XX antiproliferative; hepatotropic; nephrotropic; antiarthritic;
XX antiproliferative; cardiant; cytostatic; gene therapy; liver disease;
XX antiproliferative; disorder; renal failure; cardiovascular disorder;
XX immunological disorder; arthritis; psoriasis; congenital heart defect;
XX congestive heart failure; cancer; human; mouse; yeast; rat; fruitfly.
XX Homo sapiens.

XX WO200257460-A2.

XX 25-JUL-2002.

XX 20-DEC-2001; 2001WO-0505459.

XX 20-DEC-2001; 2001US-0256868P.

XX 30-MAR-2001; 2001US-0280186P.

XX 01-JAN-2001; 2001US-0287735P.

XX 05-JUN-2001; 2001US-0256848P.

XX 25-JUN-2001; 2001US-0304659P.

XX (BRIM) BRISTOL-MYERS SQUIBB CO.

XX Jackson DG, Feder J, Nelson T, Mintier G, Ramanathan C, Lee L,
XX Jackson DG, Feder J, Nelson T, Mintier G, Ramanathan C, Lee L,
XX Krystak S, Mccarthy P, Suchard S, Banae D;
XX WPI, 2002-599721/64.

XX Novel polynucleotides encoding human phosphatase polypeptides useful in
XX the prevention or treatment of e.g. proliferative and cardiovascular
XX disorders.

XX Disclosure; Page 174; 801pp; English.

XX The invention relates to a novel isolated nucleic acid comprising a
XX polynucleotide having a nucleotide sequence selected from 40
XX polynucleotides fully defined in the specification. The polynucleotide of
XX the invention has antiproliferative, hepatotropic, nephrotropic,

CC antiarthritic, antipsoriatic, cardiant, and cytostatic activity. The
 CC polynucleotide may have a use in gene therapy. A polynucleotide or
 CC peptide of the invention is useful for identifying modulators of its
 CC proliferating medical condition, e.g. a proliferative disorder.
 CC also useful for treating e.g. liver disease, renal failure, and
 CC disorders including arthritis and psoriasis, cardiovascular disorders
 CC such as congenital heart defects and congestive heart failure, and
 CC condition or susceptibility to a condition in a subject. The present
 CC sequence is used in the exemplification of the invention

XX Sequence 23 AA;
 XX

Query Match 100.0%; Score 52; DB 5; Length 23;
 Best Local Similarity 100.0%; Pred. No. 0.0056;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHLGAGISRS 10
 |||||
 DB 6 VHLGAGISRS 15

RESULT 2

ID ABR52380 standard; peptide; 23 AA.

XX ABR52380;

XX 19-JUN-2003 (first entry)

XX Peptide relating to the invention SEQ ID NO: 103.

XX antiproliferative; hepatotropic; nephrotropic; antiarthritic;
 XX antipsoriatic; cardiant; cytostatic; gene therapy; liver disease;
 XX proliferative disorder; renal failure; cardiovascular disorder;
 XX immunological disorder; arthritis; psoriasis; congenital heart
 XX congestive heart failure; cancer; human; mouse; yeast; rat; fruitfly.

XX Homo sapiens.

XX WO2002057460-A2.

XX 25-JUL-2002.

XX 20-DEC-2001; 2001WO-08950459.

XX 20-DEC-2000; 2000US-0256868P.

XX 30-MAR-2001; 2001US-0280186P.

XX 01-MAY-2001; 2001US-0287735P.

XX 05-JUN-2001; 2001US-0298488P.

XX 25-JUN-2001; 2001US-0304655P.

XX (BRM) BRISTOL-MYERS SQUIBB CO.

XX Jackson DG, Feder J, Nelson T, Wintner G, Ramanathan C, Lee L;
 XX B, Schuchman B, Schuchman R, Rodertud G, Bassolino D;
 XX Kryatek S, Mostee P, Suchard S, Banaas D;

XX WPI; 2002-599721/64.

XX Novel polynucleotides encoding human phosphatase polypeptides useful in
 XX the prevention or treatment of e.g. proliferative and cardiovascular
 XX disorders.

XX Disclosure, Page 129; 801pp; English.

XX The invention relates to a novel isolated nucleic acid comprising a
 XX polynucleotide having a nucleotide sequence selected from 40
 XX polynucleotides and their derivatives. The polynucleotide of
 XX antiarthritic, antipsoriatic, cardiant, and cytostatic activity. The
 XX polynucleotide may have a use in gene therapy. A polynucleotide or
 XX peptide of the invention is useful for identifying modulators of its
 XX proliferating medical condition, e.g. a proliferative disorder.

CC ameliorating a medical condition, e.g. a proliferative disorder. They are
 CC also useful for treating e.g. liver disease, renal failure, immunological
 CC disorder, arthritis, psoriasis, congenital heart defects and congestive heart failure, and
 CC cancer. A method of the invention is useful for diagnosing a pathological
 CC condition or susceptibility to a condition in a subject. The present
 CC sequence is used in the exemplification of the invention

XX Sequence 23 AA;

Query Match 100.0%; Score 52; DB 5; Length 23;
 Best Local Similarity 100.0%; Pred. No. 0.0056;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHLGAGISRS 10
 |||||
 DB 6 VHLGAGISRS 15

RESULT 3

ANU79157

ID ANU79157 standard; protein; 41 AA.

XX AAU79157;

XX 02-JUL-2002 (first entry)

XX Human EST AC007619 DSP-16 C-terminal protein sequence.

XX Human; dual-specificity phosphatase-3; DSP-16; autoimmune disease;
 XX mitogen-activated protein kinase; Akt; Duchenne muscular dystrophy;
 XX cell cycle abnormality; anchorage independent cell growth; contact inhibition;
 XX abnormal cell growth; abnormal cell proliferation; contact inhibition;
 XX cell cycle abnormality; anchorage independent cell growth; apoptosis;
 XX intercellular adhesion; DSP-16 modulator; expressed sequence tag; EST.

XX Homo sapiens.

XX WO200226997-A2.

XX 04-APR-2002.

XX 25-SEP-2001; 2001WO-US030124.

XX 26-SEP-2000; 2000US-0235487P.

XX (CBPT)- CREPTVR INC.

XX Lucche RW, Wei B;

XX WPI; 2002-315802/35.

XX New DSP-16 polypeptide, useful for identifying modulators of its
 XX activity, which can be used in the treatment of disorders such as
 XX Duchenne muscular dystrophy, or cancer.

XX Example 1; Page 50; 87pp; English.

XX The present invention relates to a new polypeptide, DSP-16, having a 665
 XX amino acid sequence. The polypeptide is identical to that having at
 XX least 50 % identical residues, which retains the ability to
 XX dephosphorylate an activated mitogen-activated protein (MAP) kinase. The
 XX invention can be used for identifying agents which modulate DSP-16
 XX activity, for identifying a proliferative disorder, for identifying a
 XX condition or susceptibility to a proliferative disorder, for identifying a
 XX inhibition of cell growth or anchorage independent growth and may display
 XX altered intercellular adhesion. The agent may modulate apoptosis, or the
 XX cell cycle. The identified modulators can be used to treat Duchenne
 XX muscular dystrophy, autoimmune disease, cancer, abnormal cell growth, abnormal
 XX cell proliferation, and cell cycle abnormalities. The present amino acid
 XX sequence represents the human EST AC007619 DSP-16 C-terminal protein
 XX sequence. This sequence was used in the methods of the invention for

C cloning and sequencing cDNA encoding the human dual-specificity

X phosphatase-3 (DSP-16) protein of the invention

X Q Sequence 41 AA; 100.0%; Score 52; DB 5; Length 140;

X Query Watch Best Local Similarity 100.0%; Pred. No. 0.01; Mismatches 0; Indels 0; Gaps 0;

X Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

X Y 1 VHCLAGISRS 10

X | | | | |

X 11 VHCLAGISRS 20

X | | | | |

X RESULT 4

X BR52404

X D ABR52404 standard; protein; 140 AA.

X X ABR52404;

X X 19-JUN-2003 (first entry)

X X Peptide relating to the invention SEQ ID NO: 134.

X X antiproliferative; hepatotropic; nephrotropic; antiarthritic;

X X antipapillary; cardiac; cytostatic; gene therapy; liver disease;

X X proliferative disorder; renal failure; cardiovascular disorder;

X X immunological disorder; arthritis; psoriasis; congenital heart defect;

X X congestive heart failure; cancer; human; mouse; yeast; rat; fruitfly.

X X Homo sapiens.

X X WO200257460-A2.

X X 25-JUL-2002.

X X 20-DEC-2000; 2001WO-US050459.

X X 30-MAR-2001; 2001US-0256868P.

X X 01-MAY-2001; 2001US-0280186P.

X X 05-JUN-2001; 2001US-0255648P.

X X 25-JUN-2001; 2001US-030465P.

X X (BR1) BRISTOL-MYERS SQUIBB CO.

X X Jackson DG, Fider J, Nelson T, Mintier G, Ramanathan C, Lee L;

X X Krysak S, Kearse P, Scharad S, Banas D;

X X WPI, 2002-599721/64.

X X Novel polynucleotides encoding human phosphatase polypeptides useful in

X X the prevention or treatment of e.g. proliferative and cardiovascular

X X disorders.

X X Disclosure; Page 164; 80pp; English.

X X The invention relates to a novel isolated nucleic acid comprising a

X X polynucleotide having a nucleotide sequence selected from 40

X X polynucleotides fully defined in the specification. The polynucleotide of

X X the invention has antiproliferative, hepatotropic, nephrotropic,

X X antipapillary, cardiac, cytostatic, gene therapy, antiproliferative or

X X polynucleotide may have a use in gene therapy. A polynucleotide or

X X polypeptide of the invention is useful for preventing, treating or

X X ameliorating a medical condition, e.g. a proliferative disorder. They are

X X useful for treating e.g. cancer, renal failure, immunological

X X disorders including heart defects and congenital heart failure, and

X X such as congenital heart defects and congestive heart failure, and

X X cancer. A method of the invention is useful for diagnosing a pathological

X X condition or susceptibility to a condition in a subject. The present

X X sequence is used in the exemplification of the invention

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QO Sequence 140 AA;

Query Watch

Best Local Similarity 100.0%; Score 52; DB 5; Length 140;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VHCLAGISRS 10

| | | | |

DB 85 VHCLAGISRS 94

| | | | |

RESULT 5

AAB66435

ID AAB66435 standard; protein; 168 AA.

X AAB66435;

XX 06-APR-2001 (first entry)

XX Human MAP-kinase phosphatase MKP-7.

XX Human; MAP-kinase; mitogen-activated protein kinase; DSP-3; cytostatic;

XX immunosuppressive; antiallergic; dual specificity phosphatase-3;

XX cell proliferation; metabolic diseases; Duchenne muscular dystrophy;

XX cancer; graft-versus-host disease; autoimmune disease; allergy; MKP-7.

XX Homo sapiens.

XX WO200102582-A1.

XX 11-JAN-2001.

XX 29-JUN-2000; 2000WO-US018207.

XX 02-JUL-1999; 98US-0142338P.

XX 07-APR-2000; 2000MC-US009185.

XX 20-APR-2000; 2000MC-US010868.

XX (CEPT-) CEPTYR INC.

XX Lucche EM, Wei B;

XX WPI, 2001-138149/149.

XX New dual-specificity phosphatase (DSP)-3 and DSP-3 alternate form

XX polypeptides, useful for identifying modulators DSP-3 or DSP-3 alternate

XX form activity, especially for treating e.g. cancer, autoimmune diseases

XX or allergies.

XX Example 1; Fig 3; 86pp; English.

XX The present sequence is given in a specification providing human dual

XX specificity phosphatase (DSP-3) and a murine DSP-3 variant polypeptide.

XX The present sequence is useful for identifying modulators of DSP-3 or

XX e.g. MAP-kinase. They may be used to treat or prevent diseases, or

XX with cell proliferation, immunosuppression, metabolic diseases, or

XX abnormal cell growth or cell cycle abnormalities. They are also useful

XX for treating diseases that modulate the activity of DSP-3. The modulators are

XX useful for treating diseases that modulate the activity of DSP-3.

XX activity, e.g. Duchenne muscular dystrophy, cancer, graft-versus-host

XX disease, autoimmune diseases, allergies, metabolic diseases, abnormal

XX cell growth, abnormal cell proliferation and cell cycle abnormalities.

XX The present sequence is useful for identifying modulators of DSP-3 or

XX cellular responses, e.g. in vivo or in vitro cell proliferation, cell

XX differentiation or survival. The present sequence was used in homology

XX studies with DSP-3 and other MAP-kinase phosphatases

XX

XX Sequence 168 AA;

Query Match

Best Local Similarity 100.0%; Score 52; DB 4; Length 168;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

B Human MAP-kinase phosphatase bVH5.
 # Human, MAP-kinase; mitogen-activated protein kinase; DSP-3; cytostatic;
 # immunosuppressive; antiallergic; dual specificity phosphatase-3;
 # human; human; human; human; human; human; human; human; human;
 # cancer; graft-versus-host disease; autoimmune disease; allergy; bVH5.
 #
 # Homo sapiens.
 # WC200102582-A1.
 # 11-JAN-2001.
 # 29-JUN-2000; 2000NO-US018207.
 # 02-JUL-1999; 98US-0142338P.
 # 07-APR-2000; 2000NO-US009185.
 # 20-APR-2000; 2000NO-US010868.
 # (CEPT-) CEPTTR INC.
 # Lucie RW, Wei B;
 # WPI, 2001-138149/14.
 # New dual-specificity phosphatase (DSP)-3 and DSP-3 alternate form
 # polypeptides, useful for identifying modulators DSP-3 or DSP-3 alternate
 # form activity, especially for treating e.g. cancer, autoimmune diseases
 # or allergies.
 # Example 1; Fig 3; 86pp; English.
 # The present sequence is given in a specification providing human dual
 # specificity phosphatase-3 (DSP-3) and a murine DSP-3 variant polypeptide.
 # The polypeptides are useful for dephosphorylating a substrate of DSP-3.
 # e.g. MAP-kinase. They may be used to treat or prevent diseases associated
 # with cell proliferation, immunosuppression, metabolic diseases, or
 # cancer, e.g. cancer, autoimmune diseases, allergy, metabolic diseases,
 # for identifying agents that modulate their activity. The modulators are
 # useful for treating disorders associated with DSP-3 or DSP-3 variant
 # activity, e.g. Duchenne muscular dystrophy, cancer, graft-versus-host
 # disease, autoimmune diseases, allergies, metabolic diseases, abnormal
 # cell proliferation, immunosuppression, metabolic diseases, abnormal
 # cellular responses, e.g. in vivo or in vitro cell proliferation,
 # differentiation or survival. The present sequence was used in homology
 # studies with DSP-3 and other MAP-kinase phosphatases
 # Sequence 170 AA;
 # Query Match 100.0%; Score 52; DB 4; Length 170;
 # Best Local Similarity 100.0%; Pred. No. 0.043;
 # Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 VHLGAGISRS 10
 b 110 VHLGAGISRS 119
 RESULT 9
 #06780
 # AAE06780 standard; protein; 170 AA.
 # AAE06780;
 # 16-OCT-2001 (first entry)
 # Human dual-specificity phosphatase (DSP) protein, bVH5.
 # Human; dual-specificity phosphatase; DSP; dual phosphorylation motif;
 # mitogen-activated protein kinase; MAP-kinase; graft-versus-host
 # disease; Duchenne muscular dystrophy; therapy; cancer; autoimmune disease;
 # allergy; metabolic disease; cell growth; cell proliferation; cytostatic;

KW cell cycle abnormality; cell differentiation; antiallergic; muscular;
 KW immunosuppressive.
 XX Homo sapiens.
 OS WC200157221-A2.
 PM 09-AUG-2001.
 PD 01-FEB-2001; 2001NO-US0031429.
 PF 02-FEB-2000; 2000US-0179886P.
 PR (CEPT-) CEPTTR INC.
 XX Lucie RW, Wei B;
 XX WPI, 2001-489887/53.
 XX New isolated dual-specificity phosphatase polypeptide for treating
 XX cancer, graft-versus-host disease, autoimmune diseases, allergies,
 XX metabolic diseases, abnormal cell growth and abnormal cell proliferation.
 XX Example 1; Fig 6; 81pp; English.

CC The present sequence is human dual-specificity phosphatase (DSP) protein,
 CC bVH5. bVH5 is used to derive a longer consensus DSP amino acid sequences
 CC member. Inactivation of mitogen-activated protein kinase (MAP-kinase)
 CC is mediated by dephosphorylation at a dual phosphorylation motif by DSP
 CC which is referred to as MAP-kinase phosphatase. An agent that modulates
 CC DSP is useful for treating a disorder selected from Duchenne muscular
 CC dystrophy, cancer, autoimmune diseases, allergy, metabolic diseases,
 CC allergies, metabolic diseases, abnormal cell growth, abnormal cell
 CC proliferation and cell cycle abnormalities. DSP is useful for identifying
 CC antibodies and other agents that inhibit DSP-12 and/or DSP-13 activity.
 CC DSP and the agents identified are useful for modulating cell in screening
 CC assays for modulators of enzyme activity and substrate binding and for
 CC dephosphorylating a substrate of DSP-12 or DSP-13

XX Sequence 170 AA;
 # Query Match 100.0%; Score 52; DB 4; Length 170;
 # Best Local Similarity 100.0%; Pred. No. 0.043;
 # Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHLGAGISRS 10
 Db 110 VHLGAGISRS 119
 RESULT 10
 #06777
 # AAE06777 standard; protein; 170 AA.
 # AAE06777;
 # 16-OCT-2001 (first entry)
 # Human dual-specificity phosphatase (DSP) protein, bVH5.
 # Human; dual-specificity phosphatase; DSP; dual phosphorylation motif;
 # mitogen-activated protein kinase; MAP-kinase; graft-versus-host disease;
 # Duchenne muscular dystrophy; therapy; cancer; autoimmune disease;
 # allergy; metabolic disease; cell growth; cell proliferation; cytostatic;
 # cell cycle abnormality; cell differentiation; antiallergic; muscular;
 # immunosuppressive.
 XX Homo sapiens.
 OS WC200157221-A2.
 PM 09-AUG-2001.

PD 09-AUG-2001.
XX
PF 01-FEB-2001; 2001MO-US003429.
PR
PR 02-FEB-2001; 2001US-0179886P.
PR
PA (CBPT-) CBPTTR INC.
XX
XX Luche RM, Wei B,
XX
XX WFI; 2001-488887/53.
XX
XX New isolated dual-specificity phosphatase polypeptide for treating
XX metabolic diseases, abnormal cell growth and abnormal cell proliferation.
XX
XX Example 1; Fig 6; 81pp; English.
XX
XX The present sequence is human dual-specificity phosphatase (DSP) protein,
XX CC PEST1. PEST1 is used to derive a longer consensus DSP amino acid
XX CC sequences motif that would be useful for the identification of new DSP
XX CC family members. Inactivation of mitogen-activated protein kinase (MAP-
XX CC kinase) by DSP which is referred to as MAP-kinase phosphatase. An agent that
XX CC modulates DSP is useful for treating a disorder selected from Duchenne
XX CC muscular dystrophy, cancer, graft-versus-host disease (GVHD), autoimmune
XX CC diseases, allergies, metabolic diseases, abnormal DS is growth, abnormal
XX CC identifying antibodies and other agents that inhibit DSP-12 and/or DSP-13
XX CC activity. DSP and the agents identified are useful for modulating cell
XX CC proliferation, differentiation and survival. DSP is useful in screening
XX CC assays for modulators of enzyme activity and substrate binding and for
XX CC dephosphorylating a substrate of DSP-12 or DSP-13
XX
XX Sequence 170 AA:
Query Match 100.0%; Score 52; DB 4; Length 170;
Best Local Similarity 100.0%; Pred No. 0.041;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy' 1 VHCLAGISHS 10
Db 110 VHCLAGISHS 119

RESULT 11
ABRS3102
ID AAB53302 standard; protein; 189 AA.
XX
XX AAB53302;
XX
XX 09-MAR-2001 (first entry)
XX
XX Human colon cancer antigen protein sequence SEQ ID NO:842.
XX
XX Human; colon cancer; colon cancer antigen; diagnosis; detection;
XX identification; cytostatic; cardioactive; neuroprotective; valvular;
XX immunomodulatory; muscular; gynecological; gastroenteric;
XX nephrotropic; antineoplastic; antibacterial; gene therapy; wound;
XX neural disorder; immune system disorder; muscular disorder;
XX infectious disease; cardiovascular disorder;
XX
XX Homo sapiens.
XX
XX WO200053551-A1.
XX
XX 21-SEP-2001.
XX
XX 08-MAR-2000; 2000MO-US005083.
XX
XX 12-MAR-1999; 95US-0124270P.
XX
XX Jackson DG, Feder J, Nelson T, Mintier G, Ramanathan C, Lee L;

PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM;
XX
XX WPI; 2000-587534/55.
XX
XX N-PSDB; ACM98059.
XX
XX Colon cancer associated gene sequences, referred to as colon cancer
XX antigens, are useful for the treatment, prevention, and diagnosis of colon
XX disorders such as colon cancer.
XX
XX Claim 11; Page 1391-1392; 2104pp; English.
XX
XX AAC97991 to AAC98765 encode the human colon cancer associated proteins,
XX CC called human colon cancer antigens, given in AAB53234 to AAB54006. The
XX CC human colon cancer antigens can have cytostatic, cardioactive, muscular;
XX CC neuroprotective, immunomodulatory, gynecological, gastroenteric, and
XX CC immunomodulatory, muscular; gynecological; gastroenteric, and
XX CC can be used in gene therapy. The colon cancer antigen polynucleotide,
XX CC proteins and antibodies to the proteins are useful for the prevention,
XX CC treatment and diagnosis of colon disorders, such as colon cancer. The
XX CC polynucleotide may be used in diagnostics and research. The proteins may
XX CC also be used to prevent diseases such as neural disorders, immune system
XX CC disorders, muscular disorders, reproductive disorders, gastrointestinal
XX CC disorders, wounds, renal disorders, infectious diseases, and
XX CC cardiovascular disorders. The proteins can be used to represent
XX CC sequences used in the simplification of the present invention
XX
XX Sequence 189 AA;
Query Match 100.0%; Score 52; DB 3; Length 189;
Best Local Similarity 100.0%; Pred No. 0.047;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy' 1 VHCLAGISHS 10
Db 99 VHCLAGISHS 108

RESULT 12
ABRS2425
ID AAB52425 standard; protein; 302 AA.
XX
XX AAB52425;
XX
XX 19-JUN-2003 (first entry)
XX
XX Protein relating to the invention SEQ ID NO: 191.
XX
XX antiproliferative; hepatotropic; nephrotropic; antiarthritic;
XX antineoplastic; cardiant; cytostatic; gene therapy; liver disease;
XX proliferative disorder; renal failure; cardiovascular disorder;
XX immunological disorder; arthritis; psoriasis; congenital heart defect;
XX congestive heart failure; cancer; human; mouse; yeast; rat; fruitfly.
XX
XX Homo sapiens.
XX
XX WO200257460-A2.
XX
XX 25-JUL-2002.
XX
XX 20-DEC-2001; 2001MO-US0050459.
XX
XX 30-DEC-2000; 2000US-0256868P.
XX
XX 10-MAR-2001; 2001US-0280186P.
XX
XX 01-MAY-2001; 2001US-0287735P.
XX
XX 05-JUN-2001; 2001US-0295848P.
XX
XX 25-JUN-2001; 2001US-0300463P.
XX
XX (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
XX Jackson DG, Feder J, Nelson T, Mintier G, Ramanathan C, Lee L;
XX

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4 protein - protein search, using sw model

on on: September 23, 2004, 14:18:59 ; Search time 16 Seconds
(without alignments)
60.120 Million cell updates/sec

file: US-09-964-277-16

after score: 52

sequence: 1 VHCLAGISRS 10

scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

sarched: 283366 seqs; 96191526 residues

initial number of hits satisfying chosen parameters: 283366

initial DB seq length: 0

aximum DB seq length: 2000000000

cat-processing: Minimum Match 0%

Listing first 1000

Listing first 45 summaries

astabase :

1: Pir78.*

2: Pir2.*

3: Pir3.*

4: Pir4.*

Pir4 No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Match	Length	DB ID	Description
1	100.0	276	2	T12496	hypothetical prote
2	100.0	276	2	T12496	hypothetical prote
3	51	198.1	619	T15969	hypothetical prote
4	49	94.2	272	T18915	hypothetical prote
5	48	92.3	226	T21380	hypothetical prote
6	48	88.5	140	T21380	hypothetical prote
7	48	88.5	140	T21380	hypothetical prote
8	46	88.5	169	T10684	probable dual spec
9	46	88.5	169	AF3412	hypothetical prote
10	46	88.5	303	T46405	hypothetical prote
11	46	88.5	314	T57126	hypothetical prote
12	46	88.5	314	T57126	hypothetical prote
13	46	88.5	367	S20590	dual specificity p
14	46	88.5	367	S24411	dual specificity p
15	46	88.5	367	S25245	dual specificity p
16	46	88.5	367	S25245	dual specificity p
17	46	88.5	394	A56115	dual specificity p
18	45	86.5	171	T136845	dual specificity p
19	45	86.5	171	T28522	probable dual spec
20	45	86.5	171	T27161	hypothetical prote
21	45	86.5	171	T27161	hypothetical prote
22	45	86.5	384	T138890	dual specificity p
23	45	86.5	590	T114339	hypothetical prote
24	45	86.5	600	T14446	hypothetical prote
25	45	86.5	807	S41339	hypothetical prote
26	45	86.5	807	S41339	hypothetical prote
27	44	84.6	165	T11545	hypothetical prote
28	44	84.6	1165	T15279	hypothetical prote
29	43	83.7	171	Q0V2H1	dual specificity p

30	43	82.7	171	A42514	dual specificity p
31	42	80.8	160	T10278	dual specificity p
32	42	80.8	160	T10278	protein tyrosine p
33	42	80.8	167	JC5581	protein tyrosine p
34	42	80.8	356	JM0049	protein-tyrosine-p
35	42	80.8	356	JM0049	protein-tyrosine-p
36	42	80.8	432	TJN0317	protein-tyrosine-p
37	42	80.8	432	TJN0317	protein-tyrosine-p
38	42	80.8	435	T14845	protein-tyrosine-p
39	42	80.8	535	TPH011	protein-tyrosine-p
40	42	80.8	535	TPH011	protein-tyrosine-p
41	42	80.8	866	P84861	protein G16A3.1 (i
42	42	80.8	934	T88191	protein R6H10.2 (i
43	41	78.8	130	T29155	hypothetical prote
44	41	78.8	220	T29155	hypothetical prote
45	41	78.8	363	S12594	protein-tyrosine-p

ALIGNMENTS

RESULT 1

T48906

protein-tyrosine-phosphatase (BC 3.1.3.48) [imported] - Chlamydomonas eugametos
Species: Chlamydomonas eugametos
C.Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 21-Jul-2000
C.Accession: T48906
R.Harting, M.A.; Sideriud, M.; Joank, C.; Hirt, H.; Walton, K.M.; Musgrave, A.
Plant J., 7, 981-988, 1995
A:Reference number: 225005; PMID:95323001; PMID:7595654
A:Accession: T48906
A:Status: preliminary; translated from GB/EMBL/DDBV
A:Molecule type: cDNA
A:Cross-references: EMBL:X77938; NID:g992593; PDB:1CNA54910.1; PID:g992594
A:Genetic: X77938
A:Experimental source: strain UTEx 10
C:Genetics:
A:Gene: Vt-PTP13
C:Keywords: phosphoric monoester hydrolase

Query Match 100.0%; Score 52; DB 2; Length 276;

Best Local Similarity 100.0%; Pred. No. 0.017; 0; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0;

1 VHCLAGISRS 10

170 VHCLAGISRS 179

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Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHCAGISRS 10

Db 265 VHCAGISRS 274

RESULT 3

T15969

C:Species: *Caenorhabditis elegans*

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C:Accession: T15969

A:Chisoid, S. the EMBL Data Library, July 1995

A:Description: The sequence of *C. elegans* cosmid F08B1.

A:Reference number: Z18439

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Accession: T15969

A:Residues: 1-619 <CHI>

A:Cross-references: EMBL:U23176; NID:g726421; PID:g726422; PIDN:AAC46719.1; CESP:F08B1.1

A:Experimental source: strain Bristol N2

A:Gene: CESP:F08B1.1

A:Insertions: 22/2; 57/1; 99/1; 160/3; 252/2; 549/3

Query Match 98.1%; Score 51; DB 2; Length 619;

Best Local Similarity 90.0%; Pred. No. 0.055; 0; Gaps 0;

Matches 9; Conservative 1; Mismatches 0; Indels 0;

QY 1 VHCAGISRS 10

Db 222 VHCAGISRS 231

RESULT 4

T18915

C:Species: *Caenorhabditis elegans*

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T18915

A:Chisoid, C. the EMBL Data Library, November 1996

A:Reference number: Z19044

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Accession: T18915

A:Residues: 1-272 <EMBL>

A:Cross-references: EMBL:Z81461; PIDN:CAB03837.1; GSPDB:GN00019; CESP:C04F12.8

A:Experimental source: clone C04F12

A:Gene: p.C04F12.8

A:Map position: 1

A:Insertions: 53/1; 84/3; 204/2

Query Match 94.2%; Score 49; DB 2; Length 272;

Best Local Similarity 90.0%; Pred. No. 0.13; 0; Gaps 0;

Matches 8; Conservative 2; Mismatches 0; Indels 0;

QY 1 VHCAGISRS 10

Db 92 VHCAGISRS 101

RESULT 5

T15969

C:Species: *Caenorhabditis elegans*

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T21380

A:Chisoid, S. the EMBL Data Library, August 1996

A:Reference number: Z18439

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Accession: T21380

A:Residues: 1-619 <CHI>

A:Cross-references: EMBL:U23176; NID:g726421; PID:g726422; PIDN:AAC46719.1; CESP:F08B1.1

A:Experimental source: strain Bristol N2

A:Gene: CESP:F08B1.1

A:Insertions: 22/2; 57/1; 99/1; 160/3; 252/2; 549/3

Query Match 98.1%; Score 51; DB 2; Length 619;

Best Local Similarity 90.0%; Pred. No. 0.055; 0; Gaps 0;

Matches 9; Conservative 1; Mismatches 0; Indels 0;

QY 1 VHCAGISRS 10

Db 222 VHCAGISRS 231

A:Reference number: Z19415

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-226 <MTL>

A:Cross-references: EMBL:Z78419; PIDN:CAB01700.1; GSPDB:GN00019; CESP:F26A3.4

A:Experimental source: clone F26A3

A:Gene: CESP:F26A3.4

A:Map position: 1

A:Insertions: 11/7; 150/3; 186/3

Query Match 92.3%; Score 48; DB 2; Length 226;

Best Local Similarity 80.0%; Pred. No. 0.083; 0; Gaps 0;

Matches 8; Conservative 2; Mismatches 0; Indels 0;

QY 1 VHCAGISRS 10

Db 96 VHCAGISRS 105

RESULT 6

T33698

C:Species: *Schizosaccharomyces pombe*

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999

C:Accession: T33698

A:Chisoid, V. J. Church, C.M.; Rajandream, M.A.; Barrell, B.G.

A:Description: The sequence of the EMBL Data Library, July 1999

A:Reference number: Z21870

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-330 <MOO>

A:Cross-references: EMBL:U03652; PIDN:CB51765.1; GSPDB:GN00067

A:Experimental source: strain 972h; cosmid c17A3

A:Gene: p1041

A:Map position: 2

Query Match 92.3%; Score 48; DB 2; Length 330;

Best Local Similarity 90.0%; Pred. No. 0.12; 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 1; Indels 0;

QY 1 VHCAGISRS 10

Db 129 VHCAGISRS 138

RESULT 7

T03074

C:Species: *Chilo iridescent* virus

C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 08-Oct-1999

C:Accession: T03074

A:Chisoid, U. Tildona, C.A.; Darai, G.

A:Description: The sequence of Chilo iridescent virus between the genome coordinates (1-235-245, 1997)

A:Reference number: Z16847; NUID:98111693; PMID:9482595

A:Accession: T03074

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Cross-references: EMBL:AF003534; NID:g2738385; PIDN:AAB94448.1; PID:g2738421

A:Map position: 2

Query Match 88.5%; Score 46; DB 2; Length 142;

Best Local Similarity 90.0%; Pred. No. 0.13; 1; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 1; Indels 0;

QY 1 VHCAGISRS 10

Db 79 VHCAGISRS 88

SULT 8
0684
Title: dual specificity phosphoprotein phosphatases (SC 3.1.3.-) 82L - Mollusum contad
Species: Mollusum contagiosum virus 1
Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jul-2000
Accession: T30684
Linkage: 270, 813-816, 1996
Title: Genome sequence of a human tumorigenic poxvirus: Prediction of specific host re
ference number: 220876; PMID:96325459; PMID:8670425
Accession: T30684
Linkage: 270, 813-816, 1996
Molecule type: DNA
Residues: 1-169 <SR>
Cross-references: EMBL:U60315; NID:G1491943; PIDD:AC55210.1; PIDD:G1492025
Name: MCM282L
Function:
Description: catalyzes the hydrolysis of peptidyl-phosphoserine, -phosphothreonine and
-phosphotyrosine. Superfamily: dual specificity phosphoprotein phosphatase DUSP3; VHL-type dual specific
phosphoric monoester hydrolase
Query Match 88.5%; Score 46; DB 2; Length 169;
Best Local Similarity 80.0%; Pred. No. 0.15;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
1 VHLGAGISRS 10
109 VHLGAGISRS 118
SULT 9
73412
Title: dual specificity phosphoprotein phosphatases (SC 3.1.3.-) 82L - Mollusum contad
Species: Mollusum contagiosum virus 1
Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
Accession: AF3412
Linkage: 270, 813-816, 1996
Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
is: Reference number: AD3252; PMID:11756688
Accession: T3412
Linkage: 270, 813-816, 1996
Molecule type: DNA
Residues: 1-169 <SR>
Cross-references: GB:AE009917; PIDD:AAU52465.1; PIDD:G7993271; G99DB:GM00190
Name: BME1284
Function:
Description: catalyzes the hydrolysis of peptidyl-phosphoserine, -phosphothreonine, and
-phosphotyrosine. Superfamily: dual specificity phosphoprotein phosphatase 1; VHL-type dual specificity
phosphoric monoester hydrolase
Query Match 88.5%; Score 46; DB 2; Length 169;
Best Local Similarity 80.0%; Pred. No. 0.15;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
1 VHLGAGISRS 10
84 INCVGAGISRS 93
SULT 10
6405
Title: dual specificity phosphoprotein phosphatases (SC 3.1.3.-) 2 - mouse
Species: Homo sapiens man
Date: 03-Nov-1995 #sequence_revision 03-Nov-1995 #text_change 24-Apr-1999
Accession: B57126
Linkage: 250, 1703-1766, 1993
Title: PAC-1: a mitogen-induced nuclear protein tyrosine phosphatase.
Reference number: A57126; PMID:93206122; PMID:7681221
Accession: B57126
Linkage: 250, 1703-1766, 1993
Molecule type: mRNA
Residues: 1-314 <SR>
Cross-references: GB:U11330
Name: GBL1330
Function:
Description: catalyzes the hydrolysis of peptidyl-phosphoserine, -phosphothreonine, and
-phosphotyrosine. Superfamily: dual specificity phosphoprotein phosphatase 1; VHL-type dual specificity
phosphoric monoester hydrolase

A>Status: Preliminary
A.Molecule type: mRNA
A.Residues: 1-303 <AA>
A.Cross-references: EMBL:AL137704
A.Genetic: GenBank
A.Citation: GenBank
A.Note: DKF2P340J321.1
Query Match 88.5%; Score 46; DB 2; Length 303;
Best Local Similarity 80.0%; Pred. No. 0.27; 1; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;
1 VHLGAGISRS 10
187 VHLGAGISRS 196
SULT 11
AS7126
Title: dual specificity phosphoprotein phosphatase (SC 3.1.3.-) 2 - human
Nucleotide names: mitogen-induced nuclear tyrosine phosphatase; phosphatase of activat
C.Species: Homo sapiens (man)
C.Date: 03-Nov-1995 #sequence_revision 02-Jul-1995 #text_change 11-Jun-1999
C.Accession: A57126
C.Linkage: 250, 1703-1766, 1993
C.Title: PAC-1: a mitogen-induced nuclear protein tyrosine phosphatase.
C.Reference number: A57126; PMID:93206122; PMID:7681221
C.Accession: A57126
C.Linkage: 250, 1703-1766, 1993
C.Molecule type: mRNA
C.Residues: 1-314 <SR>
C.Cross-references: GB:U11329; NID:G559539; PIDD:AA50779.1; PIDD:G292376
A.Name: GDB:DUSP2
A.Cross-references: GDB:139200
A.Molecule type: mRNA
A.Residues: 1-314 <SR>
A.Function:
A.Description: catalyzes the hydrolysis of peptidyl-phosphoserine, -phosphothreonine, and
-phosphotyrosine. Superfamily: dual specificity phosphoprotein phosphatase 1; VHL-type dual specificity
phosphoric monoester hydrolase
P.140-160/Region: nuclear location signal
P.180-311/Domain: VHL-type dual specificity phosphoprotein phosphatase homology <VHL>
P.257/Active site: Cys phosphorylation intermediate setatus predicted
P.263/Binding site: substrate phosphate (Arg) setatus predicted
Query Match 88.5%; Score 46; DB 1; Length 314;
Best Local Similarity 80.0%; Pred. No. 0.27;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
1 VHLGAGISRS 10
255 VHLGAGISRS 264
SULT 12
B57126
Title: dual specificity phosphatase (SC 3.1.3.-) 2 - mouse
Species: Mus musculus (house mouse)
C.Date: 03-Nov-1995 #sequence_revision 03-Nov-1995 #text_change 24-Apr-1999
C.Accession: B57126
C.Linkage: 250, 1703-1766, 1993
C.Title: PAC-1: a mitogen-induced nuclear protein tyrosine phosphatase.
C.Reference number: A57126; PMID:93206122; PMID:7681221
C.Accession: B57126
C.Linkage: 250, 1703-1766, 1993
C.Molecule type: mRNA
Residues: 1-314 <SR>
Cross-references: GB:U11330
Name: GBL1330
Function:
Description: catalyzes the hydrolysis of peptidyl-phosphoserine, -phosphothreonine, and
-phosphotyrosine. Superfamily: dual specificity phosphoprotein phosphatase 1; VHL-type dual specificity
phosphoric monoester hydrolase

1 protein - protein search, using sw model

in on: September 23, 2004, 14:18:58 , Search time 10 Seconds
(without alignments)
52,070 Million cell updates/sec

File: US-09-964-277-16

File score: 52

Sequence: 1 VHLAGIGRS 10

Indexing table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Archived: 141681 seqs, 52070155 residues

xal number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Minimum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt_v42.*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	100.0	286	1	Q39491 chlamydomon
2	52	100.0	286	1	DUSP_RAT
3	52	100.0	320	1	Q63340 rattus norv
4	52	100.0	320	1	DUSP_MOUSE
5	52	100.0	381	1	DUSP_HUMAN
6	52	100.0	381	1	DUSP_MOUSE
7	52	100.0	381	1	DUSP_RAT
8	52	100.0	625	1	Q63416 rattus norv
9	52	100.0	625	1	DUSP_HUMAN
10	52	100.0	665	1	Q91102 mus sapien
11	52	100.0	665	1	DUSP_HUMAN
12	51	98.1	619	1	Q91102 mus sapien
13	48	92.3	125	1	Q10338 caenorhabd
14	48	92.3	295	1	Q84V22 mus muscu
15	47	89.5	176	1	DUSP_HUMAN
16	47	89.5	176	1	DUSP_MOUSE
17	46	88.5	198	1	Q85297 myoxon viri
18	46	88.5	198	1	DUSP_HUMAN
19	46	88.5	314	1	Q911Y7 mus muscu
20	46	88.5	314	1	DUS2_HUMAN
21	46	88.5	359	1	Q91102 mus sapien
22	46	88.5	367	1	DUS2_HUMAN
23	46	88.5	367	1	F28562 homo sapien
24	46	88.5	375	1	Q64623 rattus norv
25	46	88.5	375	1	DUS1_RAT
26	46	88.5	395	1	Q911Y7 gallus gall
27	45	86.5	171	1	DUSP_HUMAN
28	45	86.5	171	1	DUSP_VARY
29	45	86.5	384	1	F33064 varieg viri
30	45	86.5	807	1	Q16590 homo sapien
31	44	84.6	340	1	Q94012 mus muscu
32	44	84.6	384	1	DUSC_HUMAN
33	44	84.6	482	1	Q94838 rattus norv
34	44	84.6	482	1	DUSC_RAT
35	44	84.6	482	1	Q97666 homo sapien

G6580 mus musculus
P20495 vaccinia vi
P07239 raccoon pox
P08994 human apen
Q95073 homo sapien
P34138 dictyostell
P35821 mus muscu
P20417 rattus norv
P10611 mus muscu
P18031 homo sapien
P54637 dictyostell

ALIGNMENTS

RESULT 1

ID	PTP3_CHLEU	STANDARD;	FRT;	276 AA.
DT	01-NOV-1997 (Rel. 35; Created)			
DT	01-NOV-1997 (Rel. 35; Last sequence update)			
DT	15-MAR-2004 (Rel. 43; Last annotation update)			
DB	SwissProt			
DB	UniProt			
OS	Chlamydomonas eugametos.			
OC	Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;			
OC	Chlamydomonadaceae; Chlamydomonas.			
GN	Chlamydomonas reinhardtii			
LN	Chlamydomonas reinhardtii			
RP	SEQUENCE FROM N.A. CHARACTERIZATION, AND MUTAGENESIS OF CYS-172.			
RC	STRAIN:UTEX 10;			
RC	MEDLINE:95323001; PubMed:759654;			
RA	Muscarevich A.; Scharf H.; Jomka C.; Hirt H.; Walton K.M.,			
RT	"Tyrosine phosphatase signaling in a lower plant: cell-cycle and oxidative stress-regulated expression of the Chlamydomonas eugametos			
RT	VR-PTP3 gene." 98(1995).			
CC	- FUNCTION: Could be involved in tyrosine phosphatase signaling			
CC	- pathways, having MAP-kinases as substrate.			
CC	- CATALYTIC ACTIVITY: Protein-tyrosine phosphatase + H(2)O = protein			
CC	- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +			
CC	- phosphate.			
CC	- DEVELOPMENTAL STAGE: Nondividing gametes did not express the VR-			
CC	PTP3 gene whereas synchronously dividing vegetative cells only			
CC	expressed the VR-PTP3 gene during G1-phase of the cycle.			
CC	- ION SPECIFICITY: By oxidative stress.			
CC	- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.			
CC	- NON-RECEPTOR CLASS DUAL SPECIFICITY SUBFAMILY.			
CC	TYROSINE-PROTEIN KINASE: It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is not used in any			
CC	modified and this statement is not removed, changed, or for commercial			
CC	purposes without the prior written consent of the European Bioinformatics			
CC	Centre. Send an email to license@ebi.ac.uk.			
CC	EMBL; X77538; CAA54910.1; ..			
DR	PIR; T45905; T45906.			
DR	InterPro: IPR000340; DS phosphatase.			
DR	InterPro: IPR000387; TYR phosphatase.			
DR	Pfam: PF00782; D8PC; 1.			
DR	PROSITE: PS00343; DUSP.			
DR	PROSITE: PS00343; TYR PHOSPHATASE 1; 1.			
DR	PROSITE: PS00056; TYR PHOSPHATASE 2; 1.			
DR	PROSITE: PS00056; TYR PHOSPHATASE DUAL; 1.			
KW	Hydrolase.			
FT	DOMAIN 89 276 CATALYTIC.			

MIM: 602749; C: cytoplasm; 1S8.
 GO: GO:000737; C: cytoplasm; 1S8.
 GO: GO:000472; F: protein serine/threonine phosphatase activity; 1S8.
 GO: GO:000472; F: protein tyrosine phosphatase activity; 1S8.
 GO: GO:000472; F: protein tyrosine phosphatase activity; 1S8.
 InterPro: IPR000340; DS phosphatase.
 InterPro: IPR000343; MAPK phosphatase.
 InterPro: IPR000387; TYR phosphatase.
 PRINTS: PR01764; MAPKPHOSPHATASE.
 SMART: SM00195; DSPC; 1.
 PROSITE: PS00383; TYR PHOSPHATASE 1; FALSE NEG.
 PROSITE: PS00384; TYR PHOSPHATASE 2; 1.
 PROSITE: PS00385; TYR PHOSPHATASE 3; 1.
 HYDROLASE. 209 277 PROTEIN-TYROSINE PHOSPHATASE.
 DOMAIN 209 277 PHOSPHOCYSTEINE INTERMEDIATE (BY
 ACT_SITE 232 232 HYDROLASE)
 SEQUENCE 320 AA; 35278 MW; D38765BFA9213C CR64;
 Query Match 100.0%; Score 52; DB 1; Length 320;
 Best Local Similarity 100.0%; Pred. No. 0.0061;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Y 1 VHLGAGRS 10
 D 230 VHLGAGRS 239
 RESULT 4
 JST MOUSE STANDARD; PRT; 320 AA.
 C Q3246; 28-FEB-2003 (Rel. 41, Created)
 I 28-FEB-2003 (Rel. 41, Last sequence update)
 I 28-FEB-2003 (Rel. 41, Last annotation update)
 D DSPPT.
 S Mus musculus (Mouse).
 C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 X Eukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 K NCBI_TaxID:10090;
 X N1
 P SEQUENCE FROM N.A. PubMed:12617932.
 A Stenhouse R.D., Feldman E., Grouse L.H., Derge J.G.,
 A Kleusner R.D., Collins P.S., Wagner L.H., Shenman C.M., Schuler G.D.,
 A Altschul S.F., Ziegler B.B., Buecov K.H., Scheffer C.F., Bhac N.K.,
 A Hopkins R.F., Jordan H., Moore T., Max S.J., Wang J., Hsieh F.,
 A Stenhouse R.D., Collins P.S., Wagner L.H., Shenman C.M., Schuler G.D.,
 A Stapleton M., Soares M.R., Bonaldo M.F., Cavatini T.L., Schetz T.E.,
 A Raha S., Loquellano N.A., Peters G.J., Abramo R.D., Mullaly S.J.,
 A Richards S., Weiler K.C., Hales G.R., Kozlowski J., Gay G.,
 A Villalon D.K., Murry D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 A Peasey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 A Rodriguez A.C., Grunwald J., Schmutz S., Wyer R.W.C.,
 A Butterfield J.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
 A Schercher A., Schein J.E., Jones S.J.M., Mara M.A.,
 A Stenhouse R.D., Collins P.S., Wagner L.H., Shenman C.M., Schuler G.D.,
 T human and mouse cDNA sequence analysis of more than 15,000 full-length
 T Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 C -1. CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2O) = protein
 C -1. Cysteine + phosphate.
 C -1. SUBCELLULAR LOCATION: Cytoplasmic (by similarity).
 C -1. SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
 C Non-receptor class dual specificity subfamily.
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 or send an email to license@ebi.ac.uk

C C -1- SIMILARITY: Contains 1 rhodanese domain.
C C The complete sequences of 100 new cDNA clones from brain which code
C C for a rhodanese domain.
C C DNA Res. 7:347-355 (2000).
C C -1- FUNCTION: Involved in the inactivation of MAP Kinases.
C C -1- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
C C tyrosine + phosphate.
C C -1- COFACTOR: Mg2+.
C C -1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear.
C C -1- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
C C -1- SIMILARITY: Contains 1 rhodanese domain.
C C This SWISS-PROT entry is copyright. It is produced through a collaboration
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C C entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
C C or send an email to license@isb-sib.ch).
C C EMBL; X95518; CA64772.1; -.
C C HSP; Q16828; IMKP.
C C InterPro: IPR000340; DS phosphatase.
C C InterPro: IPR008343; MAPK_phosph.
C C InterPro: IPR001763; Rhodanese-like.
C C InterPro: IPR00782; DSGP; 1.
C C PRINTS; PR01764; MAPKPHPTASE.
C C SMART; SM00195; DSGP; 1.
C C SMART; SM00450; RHOD; 1.
C C PROSITE; PS00383; TYR PHOSPHATASE 3; 1.
C C PROSITE; PS00381; TYR PHOSPHATASE 2; 1.
C C PROSITE; PS00566; TYR PHOSPHATASE 1; 1.
C C PROSITE; PS00564; TYR PHOSPHATASE_DUAL; 1.
C C W Hydrolase; Nuclear Protein.
C C DOMAIN 162 432
C C PROTEIN-TYROSINE PHOSPHATASE.
C C T DOMAIN 152 459
C C POLY-ARG.
C C T DOMAIN 555 588
C C POLY-SER.
C C T DOMAIN 559 576
C C POLY-GLY.
C C T DOMAIN 311 552
C C PRO-RICH.
C C T ACT_SITE 246 246
C C PHOSPHOCYSTEINE INTERMEDIATE BY
C C SIMILARITY.
C C Q SEQUENCE 663 AA; 68847 MW; 416F429A12C1P47C CRC64;
Query Match 100.0%; Score 52; DB 1; Length 663;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Y 1 VHLGAGRS 10
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b 244 VHLGAGRS 253
RESULT 10
USG HUMAN STANDARD; PRT; 665 AA.
D DUSG HUMAN STANDARD; PRT; 384 AA.
C Q98784; Q9C093 (Rel. 41; Created)
T 28-FEB-2003 (Rel. 41; Last sequence update)
T 10-OCT-2003 (Rel. 42; Last annotation update)
E Dual specificity protein phosphatase 16 (EC 3.1.3.48) (EC 3.1.3.16)
E Dual specificity protein phosphatase 7 (MAP Kinase
E 1) (MKG) (MKG)
E DUSP16 OR MKP7 OR KIAA1700.
S Homo sapiens (Human).
C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
C Chamaelea; Euteleostomi; Primates; Catarrhini; Hominiidae; Homo.
X NCBI_TaxID=26666;
X [1]
P SEQUENCE FROM N.A.
P MEDLINE=21486429; PubMed=11469891;
P "MKP-7", a novel mitogen-activated protein kinase phosphatase,
P functions as a shuttle protein.;
T J. Biol. Chem. 276:39002-39011 (2001).
N [2]
L SEQUENCE FROM N.A.
L MEDLINE=21486429; PubMed=11469891;
X X MEDLINE=21082332; PubMed=11214970;
X Nagase T., Kikuno R., Hattori A., Kondo Y., Okumura K., Ohara O.;
[1]

*Prediction of the coding sequences of unidentified human genes. XIX.
The complete sequences of 100 new cDNA clones from brain which code
for a rhodanese domain.
DNA Res. 7:347-355 (2000).
-1- FUNCTION: Involved in the inactivation of MAP Kinases.
-1- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
tyrosine + phosphate.
-1- COFACTOR: Mg2+.
-1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear.
-1- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
-1- SIMILARITY: Contains 1 rhodanese domain.
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or send an email to license@isb-sib.ch).
EMBL; A052156; DAB40814.1; -.
EMBL; A051487; DAB21791.1; ALT_INIT.
HSP; Q16828; IMKP.
InterPro: IPR00340; DS phosphatase.
InterPro: IPR008343; MAPK_phosph.
InterPro: IPR001763; Rhodanese-like.
InterPro: IPR00782; DSGP; 1.
PRINTS; PR01764; MAPKPHPTASE.
SMART; SM00195; DSGP; 1.
SMART; SM00450; RHOD; 1.
PROSITE; PS00383; TYR PHOSPHATASE 3; 1.
PROSITE; PS00381; TYR PHOSPHATASE 2; 1.
PROSITE; PS00566; TYR PHOSPHATASE 1; 1.
PROSITE; PS00564; TYR PHOSPHATASE_DUAL; 1.
W Hydrolase; Nuclear Protein.
DOMAIN 162 432
PROTEIN-TYROSINE PHOSPHATASE.
T DOMAIN 152 459
POLY-ARG.
T DOMAIN 555 588
POLY-SER.
T DOMAIN 559 576
POLY-GLY.
T DOMAIN 311 552
PRO-RICH.
T ACT_SITE 246 246
PHOSPHOCYSTEINE INTERMEDIATE BY
SIMILARITY.
Q SEQUENCE 665 AA; 73101 MW; 1B0953F0B460DFP CRC64;
Query Match 100.0%; Score 52; DB 1; Length 665;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Y 1 VHLGAGRS 10
|||||
b 244 VHLGAGRS 251
RESULT 11
USG HUMAN STANDARD; PRT; 384 AA.
D DUSG HUMAN STANDARD; PRT; 384 AA.
C Q98784; Q9C093 (Rel. 41; Created)
T 28-FEB-2003 (Rel. 41; Last sequence update)
T 10-OCT-2003 (Rel. 42; Last annotation update)
E Dual specificity protein phosphatase 9 (EC 3.1.3.48) (EC 3.1.3.16)
E Dual specificity protein phosphatase 4 (MAP Kinase
E 1) (MKG) (MKG)
E DUSP16 OR MKP7 OR KIAA1700.
S Homo sapiens (Human).
C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
C Chamaelea; Euteleostomi; Primates; Catarrhini; Hominiidae; Homo.
X NCBI_TaxID=26666;
X [1]
P SEQUENCE FROM N.A.
P MEDLINE=21486429; PubMed=11469891;
P "MKP-7", a novel mitogen-activated protein kinase phosphatase,
P functions as a shuttle protein.;
T J. Biol. Chem. 276:39002-39011 (2001).
N [2]
L SEQUENCE FROM N.A.
L MEDLINE=21486429; PubMed=11469891;
X X MEDLINE=21082332; PubMed=11214970;
X Nagase T., Kikuno R., Hattori A., Kondo Y., Okumura K., Ohara O.;
[1]

<X> DUSP15.
 <X> Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 <X> Mammalia; Eutheria; Sciurognathia; Muridae; Murinae; Mus.
 <X> NCBI_TaxID=10090;
 <X> NCBI_TaxID=N.A. (ISOFORM 2).
 <X> SEQUENCE FROM N.A. (ISOFORM 2).
 <X> MEDLINE=21326039; PubMed=11432789;
 <X> Aoki M., Aoyama K., Nagata M., Matsuda T.;
 <X> "A growing family of dual specificity phosphatases with low molecular
 <X> masses."; *Biochem Biophys Res Commun* 2001; 279:103-107.
 <X> [2] Biochem. 130:133-140(2001).
 <X> SEQUENCE FROM N.A. (ISOFORM 1).
 <X> MEDLINE=21671825; PubMed=11612828;
 <X> Wu X., Zhao S., Chen D., Thibault P., F., Gao J., Kisin W.H.;
 <X> "Gene expression in the developing mouse retina by EST sequencing and
 <X> microarray analysis."; *Invest Ophthalmol Vis Sci* 2001; 42:103-110.
 <X> Nucleic Acids Res. 29:4983-4993(2001).
 <X> -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = protein +
 <X> phosphate.
 <X> -1- ALTERNATIVE PRODUCTS:
 <X> Note:Alternative splicing; Named isoforms=2;
 <X> IsoId=Q8RAV2-1; Sequence=Displayed;
 <X> Note=Derived from EST data;
 <X> Name=2; Q8RAV2-2; Sequence=VSP_007294; VSP_007295;
 <X> Note=Inactive. Lacks the active site;
 <X> -1- TISSUE SPECIFICITY: Isoform 2 is highly expressed in testis.
 <X> -1- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
 <X> Non-receptor class dual specificity subfamily.
 <X> -----
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 <X> between the Swiss Institute of Bioinformatics and the EMBL outstation -
 <X> European Bioinformatics Institute. There are no restrictions on its
 <X> use, but the EMBL/EBI logo and the text "SWISS-PROT" must appear on all
 <X> reprints and this statement is not removed. Usage by and for commercial
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 <X> or send an email to licenses@isb-sib.ch).
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 <X> MD; MG1:1934928; Dup15;
 <X> InterPro: IPR000340; DG phosphatase.
 <X> InterPro: IPR000387; TKR phosphatase.
 <X> SMART; SM00195; DUSP1.
 <X> PROSITE; PS00183; TKR PHOSPHATASE 1;
 <X> PROSITE; PS0056; TKR PHOSPHATASE 2;
 <X> PROSITE; PS0054; TKR PHOSPHATASE DUAL;
 <X> DOMAIN 65 125 PROTEIN-TYROSINE INTERMEDIATE (BY
 <X> ACT SITE 88 88 PHOSPHOCYSTEINE INTERMEDIATE (BY
 <X> SIMILARITY).
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 <X> (in isoform 2).
 <X> (in isoform 2).
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 <X> Missing (in isoform 2).
 <X> NON_TPR 125 125
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 <X> Best Local Similarity 90.0%; Pred. No. 0.014; Indels 0; Gaps 0;
 <X> Matches 0; Mismatches 0;
 <X> 1 VRLGALGNS 10
 <X> 86 VRLGALGNS 95

RESULT 14
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 DT 24-FEB-2003 (24141) Created
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Dual specificity protein phosphatase 15 (EC 3.1.3.48) (EC 3.1.3.16).
 OS Homo sapiens (Human)
 OG Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Testis;
 RA Kishimoto K., Ichibashi T., Chiba Y., Fujimori K., Hiraoka S., M.,
 RA Nishi H., Matsuda S., Otsuka S., Sato H., Wakamatsu A., Ishii S.,
 RA Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
 RA Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
 RA Magatsuma M., Takahashi-Fujii A., Ohima A., Sugiyama A., Kawakami B.,
 RA Hoshino T., Kishimoto T., Kishimoto Y., Nagai K., Inagaki T.,
 RT WEDQ human cDNA sequencing project.
 SL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 [2]
 SEQUENCE FROM N.A. PubMed=1170052;
 RA Jones P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
 RA Delmas P., Stavrides G., Almeida J.P., Babbage A.K., Baguley C.L.,
 RA Bailey J., Barlow K.P., Bates K.N., Beard L.M., Beare D.M.,
 RA Beasley P., Bell G.C., Bultman A.P., Carder N.P., Carter N.P.,
 RA Chapman J.C., Clamp M.G., Clark G., Clark S.V., Clee C.M.,
 RA Clegg S., Cobley V.E., Collier R.R., Connor R.E., Corby N.R.,
 RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
 RA Engsted L., Griffin G., Hegerl R., Hendry S., Hendry S.,
 RA Gough J., Griffiths C., Griffiths M.N.D., Hall R., Hall R.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jekes K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knight A., Laird G.K., Lawlor S.,
 RA Mah V., Martin S., McCarthy J.C., McIlroy K., McMurray A.A.,
 RA Milne S.A., Mistry D., Moore M.J.P., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.L.,
 RA Phillimore B.J.C.T., Prichard S.R., Rumb R.M., Rumb R.,
 RA Raine S.P., Raine S.P., Raine S.P., Raine S.P., Raine S.P.,
 RA Smees C.D., Smith W.M., Soderlund C., Steward C.A., Sulston J.E.,
 RA Swan R.M., Symeonis N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Travers A.C., Travers A.C., Travers A.C., Travers A.C., Travers A.C.,
 RA Whitehead S.L., Whitaker P., Willet D.R., Williams S.,
 RA Rogers J., Wray F., Hubbard T., Rubin R.M., Bentley D.R., Beck S.,
 RT "The DNA sequence and comparative analysis of human chromosome 20";
 RT Nature 414:865-871(2001).
 RC TISSUE=Brain N.A. (ISOFORM 2).
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Haussler R., Smith S.J., Schaefer C.F., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wasylyuk H.,
 RA Natchenko L., Marusik K., Farer A.A., Rubin G.M., Hong L.,
 RA Stappert M., Soares M.B., Bonaldo M.F., Calavante T.E.,
 RA Bha S.S., Loppello L.N.A., Petersen K.J., Abramson R.D., Mullany S.J.,
 RA Beak S.A., McKean P.J., McKean G.J., Abramson R.D., Mullany S.J.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,
 RA Villalón D.K., Muzny D.N., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fanev J., Hulton E., Kettelman N., Nadeau A., Rodriguez S., Sanchez A.,

```

ID DUSP FOMFV STANDARD; PRT; 166 AA.
AC Q9J552;
DE 18-OCT-2001 (Rel. 40, Created)
DE 18-OCT-2003 (Rel. 40, Last sequence update)
DE 18-OCT-2003 (Rel. 40, Translation method used)
DE Probable dual specificity protein phosphatase (EC 3.1.3.48)
DE (SV 3.1.3.16).
GN FPV188
GN Non-pox virus (FPV)
OC dsRNA viruses, no RNA stage: Poxviridae; Chordopoxvirinae;
OC Avipoxvirus
OC NCBI_TaxId=10261;
OX [1]
OX [2] SEQUENCE FROM N.A.
EA MEDLINE=20193920; PubMed=10729156;
EA Afonso C.L., Tulian E.R., Lu Z., Zarak L., Kutish G.F., Rock D.L.;
EA "The genome of fowlpox virus.";
EA J. Virol. 74:3817-3831(2000).
RL -| - as well as tyrosine-protein phosphatase (by similarity) as well
CC -| - as well as serine-protein phosphatase (by similarity)
CC -| - CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2O) = protein
CC tyrosine + phosphate.
CC -| - SIMILARITY: belongs to the protein-tyrosine phosphatase family.
CC -| - non-receptor class dual specificity subfamily.
-----
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CC or send an email to licenses@sib-ch).
CC ENMF1AIP910; MF044483;
DR InterPro; IPR000340; PS_phosphatase.
DR InterPro; IPR000387; Tyr_phosphatase.
DR Pfam; PF00782; DSPC; 1.
DR SMART; SM00195; DSPC; 1.
DR PROSITE; PS00504; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00504; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS00504; TYR_PHOSPHATASE_DUAL; 1.
DR Hydrolase.
KW ACT_SITE 108 108 PHOSPHOTYROSINE INTERMEDIATE (BY
FT FT FT FT FT FT FT FT FT FT FT FT FT FT FT FT FT FT FT FT
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Query Match 90.4%; Score 47; DB 1; Length 166;
Best Local Similarity 90.0%; Pred. No. 0.03;
Patterns 0; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VHLGLASSES 10
Db 106 VHLGLASINS 115
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Search completed: September 23, 2004, 14:19:18
Job time : 11 secs

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q protein - protein search, using sw model

in on: September 23, 2004, 14:18:58 | Search time 42 seconds
75.123 Million cell updates/sec

file: US-09-964-277-16
Effect score: 1 VHLGAGRS 10
Sequence:

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

searched: 1017041 seqs, 315518202 residues
Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Missing 1182 45 summaries

- Database: SPTREMBL 25.*
- 1: sp:Archea.*
 - 2: sp:Archea.*
 - 3: sp:Archea.*
 - 4: sp:Human.*
 - 5: sp:Invertebrate.*
 - 6: sp:Mammal.*
 - 7: sp:Mammal.*
 - 8: sp:Procellariidae.*
 - 9: sp:Phase.*
 - 10: sp:Plant.*
 - 11: sp:Rodent.*
 - 12: sp:Rodent.*
 - 13: sp:Vertebrate.*
 - 14: sp:Unclassified.*
 - 15: sp:Virus.*
 - 16: sp:Bacterioph.*
 - 17: sp:Virocneop.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	52	100.0	Q800X3	gallus gall
2	52	100.0	Q8317	mus musculus
3	52	100.0	Q8312	brachydanio rerio
4	52	100.0	Q8312	brachydanio rerio
5	52	100.0	Q4128	caenorhabditis elegans
6	52	100.0	Q9163	xenopus laevis
7	52	100.0	Q9163	xenopus laevis
8	52	100.0	Q9163	xenopus laevis
9	52	100.0	Q9163	xenopus laevis
10	52	100.0	Q8551	homo sapiens
11	52	100.0	Q8551	homo sapiens
12	52	100.0	Q81V8	homo sapiens
13	52	100.0	Q81V8	homo sapiens
14	52	100.0	Q78512	homo sapiens
15	51	98.1	Q81V8	homo sapiens
16	51	98.1	Q9NRW4	homo sapiens

17	51	98.1	184	11	Q9NN11	mus musculus
18	51	98.1	241	5	Q9VW4	drosochila
19	51	98.1	300	11	Q9AG15	mus musculus
20	51	98.1	300	11	Q9AG15	mus musculus
21	51	98.1	354	4	Q8NA44	homo sapiens
22	51	98.1	355	11	Q9AG16	mus musculus
23	51	98.1	411	5	Q9VW4	drosochila
24	51	98.1	411	5	Q9VW4	drosochila
25	51	98.1	436	11	Q9PKC2	mus musculus
26	51	98.1	439	5	Q9IC35	caenorhabditis elegans
27	51	98.1	452	11	Q8LIS9	mus musculus
28	51	98.1	452	11	Q8LIS9	mus musculus
29	51	98.1	606	11	Q8T18	caenorhabditis elegans
30	51	98.1	622	11	Q9PMG5	mus musculus
31	51	98.1	657	5	Q8T19	caenorhabditis elegans
32	51	98.1	660	11	Q9T0R2	mus musculus
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37	48	92.3	327	5	Q8ICX1	drosochila
38	48	92.3	327	5	Q8ICX1	drosochila
39	48	92.3	327	5	Q8ICX1	drosochila
40	47	90.4	168	16	Q8S54	brachydanio rerio
41	47	90.4	168	16	Q8S54	brachydanio rerio
42	46	88.5	142	12	Q95737	chilo iride
43	46	88.5	142	12	Q95737	chilo iride
44	46	88.5	165	12	Q9PMK1	amsata moo
45	46	88.5	169	12	Q92429	molluscum c

ALIGNMENTS

RESULT 1

Q800X3 PRELIMINARY; PRT: 104 AA.

Q800X3 ID Q800X3

Q800X3 AC Q800X3

Q800X3 DT 01-JUN-2003 (TEMBREL. 24, Created)

Q800X3 DT 01-JUN-2003 (TEMBREL. 24, Last sequence update)

Q800X3 DB DUALSPECIFICITY PHOSPHATASE 6 (Fragment)

Q800X3 GN DUSP6

Q800X3 OS Gallus gallus (Chicken)

Q800X3 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Galliformes; Gallinae; Gallus

Q800X3 CC NEBI_TaxID=9031;

Q800X3 RN SEQUENCE FROM N.A.

Q800X3 RP R. P. Vieira C.S.L.

Q800X3 RT "Cloning of chick dual specificity phosphatase 6."

Q800X3 RL EMBL; AY207465; Acc4007.1; - phosphatase activity; IEA

Q800X3 DR GO:000470; - protein amino acid dephosphorylation; IEA

Q800X3 DR InterPro: IPR008343; - phosphatase

Q800X3 DR InterPro: IPR008343; - MAPK phosphatase

Q800X3 DR InterPro: IPR008343; - MAPK phosphatase

Q800X3 DR PRINTS: PR01764; MAPKPHATASE

Q800X3 DR PROSITE: PS00056; TYR_PHSPTASE 2.1.

Q800X3 DR PROSITE: PS00054; TYR_PHSPTASE_DUAL; 1.

Q800X3 FT NON-TER 104

Q800X3 SQ SEQUENCE 104 AA; 11748 MM; 60863CB2AB1B753 CRC64;

Query Match

Matches 10; Similarity 100.0%; Seed No. 0.0087; Indels 0; Gaps 0;

1 VHLGAGRS 10

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CC -1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
CC TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
CC -1- COMING FROM THE CC25 HOMOLOGY DOMAIN 2 A AND B (CH2
CC COMING FROM THE CH25 HOMOLOGY DOMAIN 2 A AND B (CH2
CC EMBL: U13223; AA85240.1; --
DR HSP; Q16828; MKP.
DR GO: GO:0044723; P:calcium-dependent protein serine/threonine . . ; IEA.
DR GO: GO:0016787; P:protein kinase activity; IEA.
DR GO: GO:0016787; P:tyrosine kinase activity; IEA.
DR GO: GO:0044724; P:MAP Kinase phosphatase protein serine/threonine . . ; IEA.
DR GO: GO:0017017; P:MAP Kinase phosphatase activity; IEA.
DR GO: GO:0017018; P:invariant phosphatase activity; IEA.
DR GO: GO:0003037; P:protein phosphatase type 2B activity; IEA.
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DR GO: GO:0015071; P:protein amino acid dephosphorylation; IEA.
DR GO: GO:0006470; P:protein phosphatase activity; IEA.
DR InterPro: IPR008349; MAPK phosphatase.
DR InterPro: IPR001763; Rhodanese-like.
DR InterPro: IPR00387; TYR phosphatase.
DR Pfam: PF00782; DSPC; 1. PHOSPHATASE.
DR SMART: SM00195; DSPC; 1. PHOSPHATASE.
DR SMART: SM00450; RHOD; 1.
DR PROSITE: PSS0206; RHODANES_3; 1. PALSE_NRG.
DR PROSITE: PSS0389; TYR PHOSPHATASE_2; 1.
DR PROSITE: PSS0389; TYR PHOSPHATASE_2; 1.
DR PROSITE: PSS0054; TYR PHOSPHATASE_DUAL; 1.
KW Hydrolase. 34 49 CH2 A DOMAIN.
FT DOMAIN 152 158 CH2 A DOMAIN.
FT DOMAIN 152 158 CH2 A DOMAIN.
FT DOMAIN 205 378 CATALYTIC.
FT ACT_SITE 280 290
SQ SEQUENCE 378 AA; 42036 MW; F274D4C856B783 CRC64;
Query Match 100.0%; Score 52; DB 13; Length 378;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VHLGAGISRS 10
Db 288 VHLGAGISRS 297
RESULT 7
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ID QY7219 PRELIMINARY; PRT; 382 AA.
AC QY7219; (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE MAP kinase phosphatase 3.
DE KRP3.
GN KRP3.
OS Eukaryotic gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Sarcopterygii; Actinopterygii; Ciconiiformes; Phasianidae;
OC Gallus.
OC NCBT_TaxID=9031;
CC SEQUENCE FROM N.A.
RX MEDLINE=22660508; PubMed=12766772;
FA Kawakami Y., Rodriguez-Leon J., Koch C.M., Buecher D., Itoh T.,
FA Kaya A., Ng J.X., Rodriguez-Leon J., Itoh T., Buecher D.,
FA KRP3 mediates the cellular response to FGF signalling in the
FA vertebrate limb.
RT Nat. Cell Biol. 5:513-519(2003).
RL KRP3.
RK EMBL: AF278202; AA869999.1; --
SQ SEQUENCE 382 AA; 42528 MW; 95CA9D02098A388 CRC64;

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Query Match      100.0%; Score 52; DB 13; Length 382;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHLGAGIS 10
DB 292 VHLGAGIS 301

RESULT 8
ID Q72L8 PRELIMINARY; PRT; 382 AA.
AC Q72L8
DT 01-MAR-2002 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DB MAP kinase phosphatase 3.
GN MKP3.
OS Fugu rubripes (Japanese pufferfish) (Danio rerio).
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_TaxID=7955;
DB 292 VHLGAGIS 301
RP SEQUENCE FROM N.A.
EX MEDLINE=22660508; PubMed=12766772;
RA Kawakami Y., Rodriguez-Leon J., Koth C.M., Buscher D., Itoh T.,
RA Kaya A., Ma J.K., Rodriguez-Esteban C., Takahashi S., Henrique D.,
RA Kottmann J.H., Izpisua-Belmonte J., Izpisua-Belmonte J.,
RT "Wnt3 mediates the cellular response to FGF8 signalling in the
RT vertebrate limb.";
RL Nat. Cell Biol. 5:513-519(2003).
RL ENBL; AY278203; AA70000.1; -.
SQ SEQUENCE 382 AA; 42860 MW; 50E773D7CE797BBI CRC64;

Query Match      100.0%; Score 52; DB 13; Length 382;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHLGAGIS 10
DB 290 VHLGAGIS 299

RESULT 9
ID Q7UW48 PRELIMINARY; PRT; 383 AA.
AC Q7UW48
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
GN DUSP6, specificity phosphatase 6, isoform 8.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OC NCBI_TaxID=31033;
DB 290 VHLGAGIS 299
RP SEQUENCE FROM N.A.
EX MEDLINE=22660508; PubMed=12766772;
RA Bouffard G.G., Brinkley C., Brooke S., Benjamin B., Blakeley R.W.,
RA Ayle K., Beckerton-Sternberg S.M., Benjamin B., Blakeley R.W.,
RA Ayle K., Gupta J., Ho S.-L., Idol J.R., Karlina E., Lee-Lin S.-O.,
RA Leggett R., Lin Q., Maduro Q.V., Maduro V.B., Mastello C.,
RA Shevchenko Y., Snyder B., Stentrop S., Thomas J.W., Thomas P.J.,
RA Tjongson E.E., Touchman J.W., Turgon C., Vogt J.L., Walker M.A.,
RA Wetherby K.D., Zhang L.-H., Green E.D.,
RA Wetherby K.D., Zhang L.-H., Green E.D.,
RL SLC1 Comp. Sequencing Initiative.
RL SLC1 Comp. Sequencing Initiative.
RL ENBL; AC090119; AAL40358.1; -.

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[illegible]

OC Mus musculus (Mouse)
 OC Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 [1]
 RN STRAIN=C57BL/6; TISSUE=Brain;
 RC MDL=22368257; PubMed=12477932;
 EA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 EA Krausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 EA Hawrylycz M., Rosen B., White O., Anderson D.L.,
 EA Hopkins P.F., Jordan M.A., Venter A.,
 EA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M.,
 EA Scapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
 EA Brownstein M.J., Uding T.B., Roehlyuk I.,
 EA Bonak S.A., McEwan P.J., McKee K.J.,
 EA Richards S., Worley K.C., Hale S., Garcia A.M.,
 EA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 EA Patton J.W., Heltemeser K., Kettner M., Madan A.,
 EA Blakeley R.W., Touchman J.W., Green E.D.,
 EA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 EA Kravitz S.J., Maizumi N.,
 EA Kent J.,
 ET and mouse cDNA sequences.";
 RC Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]
 RN STRAIN=C57BL/6; TISSUE=Brain;
 RC STRAIN=C57BL/6; TISSUE=Brain;
 EA Strausberg R.;
 FL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC052705; AHS2705.1; -
 SQ SEQUENCE 665 AA; 69021 MW; 916E36A893249F CRC64;

Query Match 100.0%; Score 52; DB 11; Length 665;
 Best Local Similarity 100.0%; Pred. No. 0.053;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHCLAGTSSRS 10
 DB 244 VHCLAGTSSRS 253
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RESULT 15
 F78512 PRELIMINARY; PRT; 66 AA.
 ID F78512;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 OS Dual specificity protein phosphatase homolog hMPP-R (Fragment).
 OC Bkayotata; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RN STRAIN=C57BL/6; TISSUE=Brain;
 RC TISSUE=Brain;
 EA Dayton M.D.;
 ET Multiple phosphotyrosine phosphatase mRNAs are expressed in the human
 FL PubMed=1090863; line W138; -
 FL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U07167; A047559.1; -
 DR HSPG; Q16828; IMKP.
 DR CO; CO-0008136; P:protein tyrosine/serine/threonine phosphatase...; IBA.
 DR CO; CO-0008136; P:protein tyrosine/serine/threonine phosphatase...; IBA.
 DR InterPro: IPR000340; CS phosphatase
 DR InterPro: IPR000387; TIF_Posphatase.
 DR Pfam: PF00782; DSPC; 1.
 DR PROSITE; RS00056; TTR_PHOSPHATASE_2; 1.
 DR PROSITE; RS00054; TTR_PHOSPHATASE_DUAL; 1.

FT NON TER 1
 ST NON TER 68
 SQ SEQUENCE 66 AA; 7552 MW; 3AACCB66D0D3194A CRC64;
 Query Match 98.1%; Score 51; DB 4; Length 68;
 Best Local Similarity 90.0%; Pred. No. 0.0092;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VHCLAGTSSRS 10
 DB 21 VHCLAGTSSRS 30
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Search completed: September 23, 2004, 14:21:10
 Job time : 48 secs

US-09-544-716-13

Query Match 100.0%; Score 52; DB 4; Length 168;
 Best Local Similarity 100.0%; Pred. No. 0.014; 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VCIAGISRS 10
 Db 108 VCIAGISRS 117

RESULT 3

US-09-357-921-13
 Sequence 16 Application US/09557921
 Patent No. 6551810

GENERAL INFORMATION:
 APPLICANT: Luche, Ralf M.
 TITLE OF INVENTION: DSP-10 DUAL-SPECIFICITY PHOSPHATASE
 FILE REFERENCE: 200125.416
 CURRENT APPLICATION NUMBER: US/09/557,921
 CURRENT FILING DATE: 2000-04-20
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ ID NO 13
 LENGTH: 168
 TYPE: PRT
 ORGANISM: Homo sapiens

US-09-557-921-13

Query Match 100.0%; Score 52; DB 4; Length 168;
 Best Local Similarity 100.0%; Pred. No. 0.014; 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VCIAGISRS 10
 Db 108 VCIAGISRS 117

RESULT 4

US-09-564-357-16
 Sequence 16 Application US/0956357
 Patent No. 6645753

GENERAL INFORMATION:
 APPLICANT: Luche, Ralf M.
 TITLE OF INVENTION: DSP-5 DUAL-SPECIFICITY PHOSPHATASE
 FILE REFERENCE: 200125.413
 CURRENT APPLICATION NUMBER: US/09/564,357
 CURRENT FILING DATE: 2000-04-24
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ ID NO 16
 LENGTH: 168
 TYPE: PRT
 ORGANISM: Homo sapiens

US-09-564-357-16

Query Match 100.0%; Score 52; DB 4; Length 168;
 Best Local Similarity 100.0%; Pred. No. 0.014; 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VCIAGISRS 10
 Db 108 VCIAGISRS 117

RESULT 5

US-09-619-380-15
 Sequence 15 Application US/09619380
 Patent No. 6646991
 GENERAL INFORMATION:
 APPLICANT: Luche, Ralf M.

APPLICANT: Wei, Bo
 TITLE OF INVENTION: DSP-11 DUAL SPECIFICITY PHOSPHATASE
 FILE REFERENCE: 200125.418
 CURRENT APPLICATION NUMBER: US/09/619,380
 CURRENT FILING DATE: 2000-07-19
 NUMBER OF SEQ ID NOS: 22
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ ID NO 15
 LENGTH: 168
 TYPE: PRT
 ORGANISM: Homo sapiens

US-09-619-380-15

Query Match 100.0%; Score 52; DB 4; Length 168;
 Best Local Similarity 100.0%; Pred. No. 0.014; 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VCIAGISRS 10
 Db 108 VCIAGISRS 117

RESULT 6

US-09-544-716-12
 Sequence 12 Application US/09544716
 Patent No. 6492157

GENERAL INFORMATION:
 APPLICANT: Luche, Ralf M.
 TITLE OF INVENTION: DSP-9 DUAL-SPECIFICITY PHOSPHATASE
 FILE REFERENCE: 200125.415
 CURRENT APPLICATION NUMBER: US/09/544,716
 CURRENT FILING DATE: 2000-04-10
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ ID NO 12
 LENGTH: 170
 TYPE: PRT
 ORGANISM: Homo sapiens

US-09-544-716-12

Query Match 100.0%; Score 52; DB 4; Length 170;
 Best Local Similarity 100.0%; Pred. No. 0.014; 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VCIAGISRS 10
 Db 110 VCIAGISRS 119

RESULT 7

US-09-544-716-14
 Sequence 14 Application US/09544716
 Patent No. 6492157

GENERAL INFORMATION:
 APPLICANT: Luche, Ralf M.
 TITLE OF INVENTION: DSP-9 DUAL-SPECIFICITY PHOSPHATASE
 FILE REFERENCE: 200125.415
 CURRENT APPLICATION NUMBER: US/09/544,716
 CURRENT FILING DATE: 2000-04-10
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ ID NO 14
 LENGTH: 170
 TYPE: PRT
 ORGANISM: Homo sapiens

US-09-544-716-14

Query Match 100.0%; Score 52; DB 4; Length 170;
 Best Local Similarity 100.0%; Pred. No. 0.014; 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Mismatches 0; Indels 0; Gaps 0;


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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-564-357-15

Query Match
Best Local Similarity 100.0%; Score 52; DB 4; Length 170;
Matches 10; Conservative 0; Mismatches 0; Gaps 0

QY      1 VCLAGISRS 10
DB      110 VCLAGISRS 119

RESULT 11
US-09-564-357-17
Sequence 17, Application US/09564357
Patent No. 6645753
GENERAL INFORMATION:
APPLICANT: Luche, Ralf M.
TITLE OF INVENTION: DSP-5 DUAL-SPECIFICITY PHOSPHATASE
FILE REFERENCE: 200125.413
CURRENT APPLICATION NUMBER: US/09/564,357
CURRENT FILING DATE: 2000-04-24
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17
LENGTH: 170
TYPE: PRT
ORGANISM: Homo sapiens
US-09-564-357-17

Query Match
Best Local Similarity 100.0%; Score 52; DB 4; Length 170;
Matches 10; Conservative 0; Mismatches 0; Gaps 0

QY      1 VCLAGISRS 10
DB      110 VCLAGISRS 119

RESULT 12
US-09-564-357-18
Sequence 18, Application US/09564357
Patent No. 6645753
GENERAL INFORMATION:
APPLICANT: Luche, Ralf M.
TITLE OF INVENTION: DSP-11 DUAL SPECIFICITY PHOSPHATASE
FILE REFERENCE: 200125.418
CURRENT APPLICATION NUMBER: US/09/564,357
CURRENT FILING DATE: 2000-07-19
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 18
LENGTH: 170
TYPE: PRT
ORGANISM: Homo sapiens
US-09-564-357-18

Query Match
Best Local Similarity 100.0%; Score 52; DB 4; Length 170;
Matches 10; Conservative 0; Mismatches 0; Gaps 0

QY      1 VCLAGISRS 10
DB      110 VCLAGISRS 119

RESULT 13
US-09-564-357-19
Sequence 19, Application US/09564357
Patent No. 6645753
GENERAL INFORMATION:
APPLICANT: Luche, Ralf M.
TITLE OF INVENTION: DSP-5 DUAL-SPECIFICITY PHOSPHATASE
FILE REFERENCE: 200125.413
CURRENT APPLICATION NUMBER: US/09/564,357
CURRENT FILING DATE: 2000-04-24
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 19
LENGTH: 170
TYPE: PRT
ORGANISM: Homo sapiens
US-09-564-357-19

Query Match
Best Local Similarity 100.0%; Score 52; DB 4; Length 170;
Matches 10; Conservative 0; Mismatches 0; Gaps 0

QY      1 VCLAGISRS 10
DB      110 VCLAGISRS 119

RESULT 14
US-09-564-357-20
Sequence 20, Application US/09564357
Patent No. 6645753
GENERAL INFORMATION:
APPLICANT: Luche, Ralf M.
TITLE OF INVENTION: DSP-11 DUAL SPECIFICITY PHOSPHATASE
FILE REFERENCE: 200125.418
CURRENT APPLICATION NUMBER: US/09/564,357
CURRENT FILING DATE: 2000-07-19
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 20
LENGTH: 170
TYPE: PRT
ORGANISM: Homo sapiens
US-09-564-357-20

Query Match
Best Local Similarity 100.0%; Score 52; DB 4; Length 170;
Matches 10; Conservative 0; Mismatches 0; Gaps 0

QY      1 VCLAGISRS 10
DB      110 VCLAGISRS 119

RESULT 15
US-09-564-357-21
Sequence 21, Application US/09564357
Patent No. 6645753
GENERAL INFORMATION:
APPLICANT: Luche, Ralf M.
TITLE OF INVENTION: DSP-5 DUAL-SPECIFICITY PHOSPHATASE
FILE REFERENCE: 200125.413
CURRENT APPLICATION NUMBER: US/09/564,357
CURRENT FILING DATE: 2000-04-24
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 21
LENGTH: 170
TYPE: PRT
ORGANISM: Homo sapiens
US-09-564-357-21

Query Match
Best Local Similarity 100.0%; Score 52; DB 4; Length 170;
Matches 10; Conservative 0; Mismatches 0; Gaps 0

QY      1 VCLAGISRS 10
DB      110 VCLAGISRS 119

RESULT 16
US-09-564-357-22
Sequence 22, Application US/09564357
Patent No. 6645753
GENERAL INFORMATION:
APPLICANT: Luche, Ralf M.
TITLE OF INVENTION: DSP-11 DUAL SPECIFICITY PHOSPHATASE
FILE REFERENCE: 200125.418
CURRENT APPLICATION NUMBER: US/09/564,357
CURRENT FILING DATE: 2000-07-19
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 22
LENGTH: 170
TYPE: PRT
ORGANISM: Homo sapiens
US-09-564-357-22

Query Match
Best Local Similarity 100.0%; Score 52; DB 4; Length 170;
Matches 10; Conservative 0; Mismatches 0; Gaps 0

QY      1 VCLAGISRS 10
DB      110 VCLAGISRS 119

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US-09-619-380-16
 ; Sequence 16, Application US/09619380
 ; Patent No. 6649391
 ; GENERAL INFORMATION:
 ; APPLICANT: Lucite, Ralf M.
 ; APPLICANT: Lucite, Ralf M.
 ; TITLE OF INVENTION: DSP-11 DUAL SPECIFICITY PHOSPHATASE
 ; FILE REFERENCE: 200145-418
 ; CURRENT APPLICATION NUMBER: US/09/619,380
 ; PRIORITY DATE: 2000-07-19
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 16
 ; LENGTH: 170
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-619-380-16

Query Match 100.0%; Score 52; DB 4; Length 170;
 Best Local Similarity 100.0%; Positives 60.14%; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0

Qy 1 VNCLAGISRS 10
 Db 110 VNCLAGISRS 119

RESULT 14
 US-09-494-2
 ; Sequence 2, Application US/09816494
 ; Patent No. 6664089
 ; GENERAL INFORMATION:

APPLICANT: Meyers, Rachel A.
 ; TITLE OF INVENTION: 3D AND 2D 1117, NOVEL DUAL SPECIFICITY
 ; FILE REFERENCE: 10448-030002
 ; CURRENT APPLICATION NUMBER: US/09/816,494
 ; PRIORITY DATE: 2000-03-23
 ; PRIOR APPLICATION NUMBER: 2000-03-24
 ; PRIOR FILING DATE: 2000-03-24
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 665
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-816-494-2

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 Best Local Similarity 100.0%; Positives 6.05%; Indels 0; Gaps 0;
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Qy 1 VNCLAGISRS 10
 Db 242 VNCLAGISRS 251

RESULT 15
 US-09-045-973-8
 ; Sequence 8, Application US/09045973
 ; Patent No. 6165767
 ; GENERAL INFORMATION:

APPLICANT: Lul, Preeti
 ; APPLICANT: Lul, Preeti
 ; APPLICANT: Yue, Henry
 ; APPLICANT: Corley, Neil C.
 ; APPLICANT: Guegler, Karl J.
 ; APPLICANT: Guegler, Karl J.
 ; TITLE OF INVENTION: PROTEIN PHOSPHATASE RELATED MOLECULES
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; SRIKANTH, 1174
 ; STREET, Palo Alto
 ; CITY, Palo Alto

STATE: California
 COUNTRY: USA
 ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; HARDWARE: 80486, 386, 486, Pentium
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/045,973
 ; FILING DATE: Filled Herewith
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BULL
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PP-0491 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (650) 855-0555
 ; TELEFAX: (650) 845-4186
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 145 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; INVERSE SOURCE:
 ; CLONE: 1495338
 ; CLONE: 1495338
 US-09-045-973-8

Query Match 92.3%; Score 48; DB 3; Length 226;
 Best Local Similarity 89.8%; Indels 0;
 Matches 8; Conservative 2; Mismatches 0; Gaps 0;

Qy 1 VNCLAGISRS 10
 Db 96 VNCLAGISRS 105

Search completed: September 23, 2004, 14:21:56
 Job time: 19 secs

4 protein - protein search, using sw model

on: September 23, 2004, 14:21:14 ; Search time 129 Seconds
(without alignments)
24,927 Million cell updates/sec

file: US-09-964-277-16

blast score: 52

sequence: 1 VHCLAGISRS 10

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ost-processing: Minimum Match 0%

Listing first 45 summaries

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- 3: /cgn2_6/prodata/2/pubpaas/US06_NEW_PUB.pep.*
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- 9: /cgn2_6/prodata/2/pubpaas/US09_PUBCOMB.pep.*
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Pred No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	52	100.0	0	9	US-09-964-277-16
3	52	100.0	155	9	US-09-964-277-6
4	52	100.0	155	9	US-09-964-277-7
5	52	100.0	155	9	US-09-964-277-6
6	52	100.0	155	9	US-09-964-277-6
7	52	100.0	155	9	US-09-964-277-4
8	52	100.0	156	9	US-09-964-277-4
9	52	100.0	156	9	US-09-964-277-4
10	52	100.0	167	14	US-10-314-356-13
11	52	100.0	167	14	US-10-314-356-13
12	52	100.0	168	9	US-09-964-277-9
13	52	100.0	168	12	US-10-655-073-15
14	52	100.0	168	14	US-10-314-058-13
15	52	100.0	168	14	US-10-405-808-15

Sequence 12, Appl
Sequence 15, Appl
Sequence 23, Appl
Sequence 26, Appl
Sequence 11, Appl
Sequence 14, Appl
Sequence 16, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 842, App
Sequence 842, App
Sequence 33, Appl
Sequence 54, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 699, App
Sequence 258, App
Sequence 700, App
Sequence 2, Appl
Sequence 2, Appl
Sequence 680, App
Sequence 681, App
Sequence 14, Appl
Sequence 14, Appl
Sequence 3312, Ap

ALIGNMENTS

US-09-964-277-16
Sequence 16, Application US/09964277
Sequence 16, Application US/09964277
GENERAL INFORMATION: 1710A1
APPLICANT: Luche, Ralf M.
APPLICANT: Wei, Bo
TITLE OF INVENTION: DSP-15 DUAL-SPECIFICITY PHOSPHATASE
PUBLICATION NO: 43
CURRENT APPLICATION NUMBER: US/09/964,277
CURRENT FILING DATE: 2001-09-25
NUMBER OF SEQ ID NOS: 22
TOPICS: 1, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22
SEQ ID NOS: 1, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22
LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens
US-09-964-277-16

Query Match 100.0%; Score 52; DB 9; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.0066; Mismatches 0; Indels 0; Gaps 0;

Matches 10; Conservative 0;

QY 1 VHCLAGISRS 10

DB 1 VHCLAGISRS 10

RESULT 2

US-09-964-277-13

Sequence 13, Application US/09964277

Patent No. US20020137170A1

APPLICANT: Luche, Ralf M.

APPLICANT: Wei, Bo

TITLE OF INVENTION: DSP-16 DUAL-SPECIFICITY PHOSPHATASE

FILE REFERENCE: 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22

CURRENT APPLICATION NUMBER: US/09/964,277

```

; CURRENT FILING DATE: 2001-09-25
; INVENTOR: LUCHE, RAIF M.
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 41
; SEQ ID NO 13
; ORGANISM: Homo sapiens
US-09-964-277-13

Query Match 100.0%; Score 52; DB 9; Length 41;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VCLIGASIS 10
Db 11 VCLIGASIS 20

RESULT 3
US-09-964-277-6
; Sequence 6, Application US/09964277
; Patent No. US20020137170A1
; GENERAL INFORMATION:
; APPLICANT: Lucche, Raif M.
; TITLE OF INVENTION: DSP-16 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.434
; CURRENT APPLICATION NUMBER: US/09/964,277
; CURRENT FILING DATE: 2001-09-25
; NUMBER OF SEQ IDS: 22
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 155
; TYPE: PAT
; ORGANISM: Homo sapiens
US-09-955-732-6

Query Match 100.0%; Score 52; DB 9; Length 155;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VCLIGASIS 10
Db 96 VCLIGASIS 105

RESULT 6
US-09-964-277-3
; Sequence 3, Application US/09964277
; Patent No. US20020137170A1
; GENERAL INFORMATION:
; APPLICANT: Lucche, Raif M.
; TITLE OF INVENTION: DSP-16 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.434
; CURRENT APPLICATION NUMBER: US/09/964,277
; CURRENT FILING DATE: 2001-09-25
; NUMBER OF SEQ IDS: 105
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 156
; TYPE: PAT
; ORGANISM: Homo sapiens
US-09-964-277-3

Query Match 100.0%; Score 52; DB 9; Length 156;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VCLIGASIS 10
Db 97 VCLIGASIS 106

RESULT 7
US-09-964-277-4
; Sequence 4, Application US/09964277
; Patent No. US20020137170A1
; GENERAL INFORMATION:
; APPLICANT: Lucche, Raif M.
; TITLE OF INVENTION: DSP-16 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.434
; CURRENT APPLICATION NUMBER: US/09/964,277
; CURRENT FILING DATE: 2001-09-25
; NUMBER OF SEQ IDS: 106
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 156
; TYPE: PAT
; ORGANISM: Homo sapiens
US-09-964-277-7

Query Match 100.0%; Score 52; DB 9; Length 155;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VCLIGASIS 10
Db 96 VCLIGASIS 105

RESULT 4
US-09-964-277-7
; Sequence 7, Application US/09964277
; Patent No. US20020137170A1
; GENERAL INFORMATION:
; APPLICANT: Lucche, Raif M.
; TITLE OF INVENTION: DSP-16 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.434
; CURRENT APPLICATION NUMBER: US/09/964,277
; CURRENT FILING DATE: 2001-09-25
; NUMBER OF SEQ IDS NOS: 22
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 155
; TYPE: PAT
; ORGANISM: Homo sapiens
US-09-964-277-7

Query Match 100.0%; Score 52; DB 9; Length 155;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VCLIGASIS 10
Db 96 VCLIGASIS 105

```

ORGANISM: Homo sapiens

-09-964-277-4

Query Match 100.0%; Score 52; DB 9; Length 156;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 VHCLAGISRS 10
|||||
97 VHCLAGISRS 106

SUBT 8

-09-955-732-3
Sequence 3, Application US/09955732
Publication No. US20020182203A1

GENERAL INFORMATION:
APPLICANT: Luche, Ralf M.

TITLE OF INVENTION: DSP-15 DUAL-SPECIFICITY PHOSPHATASE
FILE REFERENCE: 200125.433
CURRENT FILING DATE: US/09/955.732
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 156
LENGTH: 156
TYPE: PRT

ORGANISM: Homo sapiens

-09-955-732-3

Query Match 100.0%; Score 52; DB 9; Length 156;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 VHCLAGISRS 10
|||||
97 VHCLAGISRS 106

RESULT 9

-09-955-732-4
Sequence 4, Application US/09955732
Publication No. US20020182203A1

GENERAL INFORMATION:
APPLICANT: Luche, Ralf M.

TITLE OF INVENTION: DSP-15 DUAL-SPECIFICITY PHOSPHATASE
FILE REFERENCE: 200125.433
CURRENT FILING DATE: US/09/955.732
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 156
LENGTH: 156
TYPE: PRT

ORGANISM: Homo sapiens

-09-955-732-4

Query Match 100.0%; Score 52; DB 9; Length 156;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 VHCLAGISRS 10
|||||
97 VHCLAGISRS 106

RESULT 10

-09-955-732-13
Sequence 13, Application US/09955732
Publication No. US20020182203A1

GENERAL INFORMATION:
APPLICANT: Luche, Ralf M.

APPLICANT: Luche, Ralf M.
TITLE OF INVENTION: DSP-10 DUAL-SPECIFICITY PHOSPHATASE
FILE REFERENCE: 200125.433
CURRENT FILING DATE: US/10/346.356
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 117
LENGTH: 167
TYPE: PRT
ORGANISM: Homo sapiens
US-10-346-356-13

Query Match 100.0%; Score 52; DB 14; Length 167;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 VHCLAGISRS 10
|||||

108 VHCLAGISRS 117

RESULT 11

-09-775-925-24
Sequence 24, Application US/09775925
Publication No. US20020182203A1

GENERAL INFORMATION:
APPLICANT: Luche, Ralf M.

TITLE OF INVENTION: DSP-13 AND DSP-13 DUAL-SPECIFICITY
PHOSPHATASES
FILE REFERENCE: 200125.420
CURRENT FILING DATE: US/09/775.925
CURRENT FILING DATE: 2001-02-01
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 24
LENGTH: 168
TYPE: PRT

ORGANISM: Homo sapiens

-09-775-925-24

Query Match 100.0%; Score 52; DB 9; Length 168;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 VHCLAGISRS 10
|||||

108 VHCLAGISRS 117

RESULT 12

-09-847-519A-9
Sequence 9, Application US/09847519A
Patent No. US20020102693A1

GENERAL INFORMATION:
APPLICANT: Luche, Ralf M.

TITLE OF INVENTION: DSP-14 DUAL-SPECIFICITY PHOSPHATASE
FILE REFERENCE: 200125.422
CURRENT APPLICATION NUMBER: US/09/847.519A
CURRENT FILING DATE: 2001-05-01
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 9
LENGTH: 166
TYPE: PRT

ORGANISM: Homo sapiens

-09-847-519A-9

Query Match 100.0%; Score 52; DB 9; Length 166;
Best Local Similarity 100.0%; Pred. No. 0.11;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VRLAGISRS 10
 |||||
 Db 108 VRLAGISRS 117

RESULT 13

US-10-405-073-15
 Seq ID NO 15
 Application US/10655073
 Publication No. US2004004141A1
 GENERAL INFORMATION:
 APPLICANT: Luche, Ralf M.
 TITLE OF INVENTION: DSP-11 DUAL-SPECIFICITY PHOSPHATASE
 FILE REFERENCE: 200125.418C1
 CURRENT APPLICATION NUMBER: US/10/655,073
 CURRENT FILING DATE: 2003-09-04
 SOFTWARE: PARTSEQ for Windows Version 4.0
 SEQ ID NO 15
 LENGTH: 168
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-655-073-15

Query Match 100.0%; Score 52; DB 12; Length 168;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VRLAGISRS 10
 |||||
 Db 108 VRLAGISRS 117

RESULT 14

US-10-314-058-13
 Application US/10314058
 Publication No. US2003011945A1
 GENERAL INFORMATION:
 APPLICANT: Luche, Ralf M.
 TITLE OF INVENTION: DSP-9 DUAL-SPECIFICITY PHOSPHATASE
 FILE REFERENCE: 200125.415C1
 CURRENT APPLICATION NUMBER: US/10/314,058
 CURRENT FILING DATE: 2002-12-05
 SOFTWARE: PARTSEQ for Windows Version 4.0
 SEQ ID NO 13
 LENGTH: 168
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-314-058-13

Query Match 100.0%; Score 52; DB 14; Length 168;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VRLAGISRS 10
 |||||
 Db 108 VRLAGISRS 117

RESULT 15

US-10-405-808-15
 Application US/10405808
 Publication No. US2003017582A1
 GENERAL INFORMATION:
 APPLICANT: Luche, Ralf M.
 TITLE OF INVENTION: DSP-4 DUAL-SPECIFICITY PHOSPHATASE
 FILE REFERENCE: 200125.410C1
 CURRENT APPLICATION NUMBER: US/10/405,808

; CURRENT FILING DATE: 2003-04-01
 ; SOFTWARE: PARTSEQ for Windows Version 4.0
 ; SEQ ID NO 15
 ; LENGTH: 168
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-405-808-15

Query Match 100.0%; Score 52; DB 14; Length 168;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 VRLAGISRS 10
 |||||
 Db 108 VRLAGISRS 117

Search completed: September 23, 2004, 14:32:40
 Job time : 139 secs